

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:12:47 ; Search time 23 Seconds

(without alignments)  
710.508 Million cell updates/sec

Title: US-09-939-484-4

Perfect score: 2042  
Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTFRLGIMKRSSV 394

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	1	CIW3_HUMAN
2	1850.5	90.6	411	1	CIW3_RAT
3	1840.5	90.1	409	1	CIW3_MOUSE
4	1116	54.7	374	1	CIW9_HUMAN
5	1069.5	52.4	365	1	CIW9_CAVPO
6	370	18.1	411	1	CIW2_MOUSE
7	364	17.8	426	1	CIW2_MOUSE
8	349.5	17.1	538	1	CIW2_MOUSE
9	349.5	17.1	538	1	CIW2_MOUSE
10	329.5	16.1	393	1	CIW4_HUMAN
11	326.5	16.0	398	1	CIW4_MOUSE
12	320.5	15.7	336	1	CIW1_HUMAN
13	319	15.6	336	1	CIW1_HUMAN
14	318.5	15.6	336	1	CIW1_MOUSE
15	295.5	14.5	313	1	CIW6_HUMAN
16	261.5	12.8	1001	1	ORL1_MOUSE
17	259.5	12.7	335	1	TRK8_MOUSE
18	224	11.0	307	1	CIW7_HUMAN
19	221	10.8	307	1	CIW8_MOUSE
20	170	8.3	691	1	TRK1_MOUSE
21	112.5	5.5	490	1	CIW1_MOUSE
22	100	4.9	694	1	CIW2_MOUSE
23	99.5	4.9	1174	1	CIW2_MOUSE
24	98	4.8	1174	1	CIW2_MOUSE
25	97.5	4.8	228	1	TRK1_MOUSE
26	97.5	4.8	432	1	TRK1_MOUSE
27	96.5	4.7	449	1	TRK1_MOUSE
28	94.5	4.6	209	1	TRK1_MOUSE
29	94.5	4.6	385	1	TRK1_MOUSE
30	94.5	4.6	449	1	TRK1_MOUSE
31	94.5	4.6	647	1	TRK1_MOUSE
32	94	4.6	262	1	TRK1_MOUSE
33	94	4.6	287	1	TRK1_MOUSE

34	94	4.6	1159	1	HERG_HUMAN	Q12809 homo sapien
35	93.5	4.6	285	1	MC2C_ARATH	P30302 arabidopsis
36	93	4.6	529	1	CIW6_HUMAN	P17658 homo sapien
37	93	4.6	602	1	CIW5_RAT	P19024 ratuus norv
38	92.5	4.5	565	1	DSBD_ECO57	P58162 escherichia
39	92.5	4.5	653	1	CIW4_HUMAN	P22459 homo sapien
40	92.5	4.5	655	1	CIW4_RAT	P15385 ratuus norv
41	92.5	4.5	685	1	FZD8_MOUSE	O61091 mus musculu
42	92	4.5	451	1	IFR1_HUMAN	O00458 homo sapien
43	92	4.5	598	1	CIW5_RABIT	P50638 oryctolagus
44	91.5	4.5	660	1	CIW4_BOVIN	O05037 bos tauru
45	91.5	4.5	1581	1	VGIP_BEV	P23052 berne virus

## ALIGNMENTS

RESULT 1	ID	CIW3_HUMAN	STANDARD:	PRT:	394 AA.
AC	014649				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Potassium channel subfamily K member 3 (acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K+ channel).				
GN	KCNK3 OR TASK.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE=97459932; PubMed=9312005;				
RA	Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;				
RT	"TASK, a human background K+ channel to sense external pH variations near physiological pH.";				
RT	EMBO J. 16:5464-5471(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Heart;				
RA	Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H.,				
RT	Goldstein S.A.N.;				
RT	"Proton block and voltage-gating are potassium-dependent in the cardiac leak channel Kcnk3.";				
RT	Submitted (May-1998) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	ACTIVATION.				
RX	MEDLINE=99254548; PubMed=10321245;				
RA	Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;				
RT	"Inhalational anesthetics activate two-pore-domain background K+ channels.";				
RT	Nat. Neurosci. 2:422-426(1999).				
CC	- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE. BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.				
CC	- SUBCELLULAR LOCATION: Integral membrane protein (potential).				
CC	- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN, LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SMALL INTESTINE AND COLON.				
CC	- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY HALOTHANE AND ISOFLURANE.				
CC	- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.				
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CC EMBL: AF006823; AAC5177.1; -

DR EMBL: AF065163; AAC29340.1; -

DR Genew; HENC:6278; KCNK3.

DR MIM; 603220; -

DR InterPro: IPR003280; K+channel\_2pore.

DR InterPro: IPR001622; K+channel\_pore.

DR InterPro: IPR000636; M+channel\_nlg.

DR InterPro: IPR003092; TASK\_channel.

DR Pfam; PF00520; Ion\_trans.1.

DR PRINTS; PR01333; 2PORECHANNEL.

DR PRINTS; PR01095; TASKCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Potassium transport;

KM Glycoprotein.

FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 9 29 POTENTIAL.

FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).

FT TRANSSEM 108 128 POTENTIAL.

FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 159 179 POTENTIAL.

FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).

FT TRANSSEM 223 243 POTENTIAL.

FT DOMAIN 244 394 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).

SO SEQUENCE 394 AA; 43518 MW; 9FAC8266F615EB7 CRC64;

Query Match 100.0%; Score 2042; DB 1; Length 394;

Best Local Similarity 100.0%; Pred. No. 1e-153;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELROQLERARVNLSCGYE 60

DB 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELROQLERARVNLSCGYE 60

QY 61 ELERVVLRKPKHAGVQWRPAGSFYAIYVITIGGHAAPSTDGKVCMEFYALLGIP 120

DB 61 ELERVVLRKPKHAGVQWRPAGSFYAIYVITIGGHAAPSTDGKVCMEFYALLGIP 120

QY 121 TLVWFOSLGRINTLVRYLLHRAKKGIGMRADVSNANVLLGFSCISITLCIGAAAFSH 180

DB 121 TLVWFOSLGRINTLVRYLLHRAKKGIGMRADVSNANVLLGFSCISITLCIGAAAFSH 180

QY 181 YEHMTFFQAYVYCFITLTITIGFDYVALOKDALOTOPQVAVSFYIILGLTVIGAF 240

DB 181 YEHMTFFQAYVYCFITLTITIGFDYVALOKDALOTOPQVAVSFYIILGLTVIGAF 240

QY 241 LVLVLRMTNNAEEDKRDARHALLTRNGAGGGGSAHTTDTASTAAGGGGFRNRY 300

DB 241 LVLVLRMTNNAEEDKRDARHALLTRNGAGGGGSAHTTDTASTAAGGGGFRNRY 300

QY 301 AEVLHFOSMSCLMYRSREKLOYISIPMLIPROLDSTDCVQSHSSGGGGRYSDPSSR 360

DB 301 AEVLHFOSMSCLMYRSREKLOYISIPMLIPROLDSTDCVQSHSSGGGGRYSDPSSR 360

QY 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

DB 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 2

CIW3\_RAT STANDARD; PRT; 411 AA.

AC 054912;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K+ channel).

GN KCNK3 OR TASK.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_Taxid=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Cerebellum;

RX MEDLINE=98099797; PubMed=9437008;

RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forsythe J.R., Yost C.S.;

RT "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum".

RU J. Neurosci. 18:868-877(1998).

CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL. PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART, MODERATE EXPRESSION IN LUNG AND BRAIN, LOW LEVELS IN LIVER, KIDNEY AND SKELETAL MUSCLE.

CC -1- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BUPRYACINE AND PHENTOLIN. ACTIVATED BY PROTEIN KINASE A.

CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

CC -----

CC EMBL: AF03184; AAC39952.1; -

DR InterPro: IPR003280; K+channel\_2pore.

DR InterPro: IPR001622; K+channel\_pore.

DR InterPro: IPR000636; M+channel\_nlg.

DR InterPro: IPR003092; TASK\_channel.

DR Pfam; PF00520; Ion\_trans.1.

DR PRINTS; PR01333; 2PORECHANNEL.

DR PRINTS; PR01095; TASKCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Potassium transport;

KM Glycoprotein.

FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 9 29 POTENTIAL.

FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).

FT TRANSSEM 108 128 POTENTIAL.

FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 159 179 POTENTIAL.

FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).

FT TRANSSEM 223 243 POTENTIAL.

FT DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).

SO SEQUENCE 411 AA; 45276 MW; D277801603E2B5 CRC64;

Query Match 90.6%; Score 1850.5; DB 1; Length 411;

Best Local Similarity 88.3%; Pred. No. 1.3e-138;

Matches 363; Conservative 8; Mismatches 23; Indels 17; Gaps 2;

QY 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELROQLERARVNLSCGYE 60

DB 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELROQLERARVNLSCGYE 60

QY 61 ELERVVLRKPKHAGVQWRPAGSFYAIYVITIGGHAAPSTDGKVCMEFYALLGIP 120

DB 61 ELERVVLRKPKHAGVQWRPAGSFYAIYVITIGGHAAPSTDGKVCMEFYALLGIP 120

QY 121 TLVWFOSLGRINTLVRYLLHRAKKGIGMRADVSNANVLLGFSCISITLCIGAAAFSH 180

DB 121 TLVWFOSLGRINTLVRYLLHRAKKGIGMRADVSNANVLLGFSCISITLCIGAAAFSH 180

QY 181 YEHMTFFQAYVYCFITLTITIGFDYVALOKDALOTOPQVAVSFYIILGLTVIGAF 240



DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Potassium channel subfamily K member 9 (acid-sensitive potassium  
 GN channel protein TASK-3) (TWIK-related acid-sensitive K<sup>+</sup> channel 3).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=20287530; PubMed=10747866;  
 RA Rajan S., Wilschmeyer E., Liu G.X., Prestig-Mueller R., Daut J.,  
 RA Karschin A., Derst C.;  
 RT "TASK-3, a novel tandem pore domain acid-sensitive K<sup>+</sup> channel. An  
 RT extracellular histidine as pH sensor.";  
 RL J. Biol. Chem. 275:16650-16657(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=20499203; PubMed=11042359;  
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,  
 RA Kelsell R.E., Muddock P.R., Goddard A.D., Rennie G.I., Gloger I.S.;  
 RT "Cloning, localization and functional expression of a novel human,  
 RT cerebellum specific, two pore domain potassium channel.";  
 RL Brain Res. Mol. Brain Res. 82:74-83(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Girard C., Lesage F., Tinel N., Lazdunski M.;  
 RT "Human Task-3, a novel 2p domain potassium channel related to Task.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina M., Pountney D.,  
 RA Coetzee W., Rudy B.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
 CC CHANNEL PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: MAINLY FOUND IN THE CEREBELLUM.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC -----  
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 CC -----  
 DR EMBL: AF212829; AAF63708.1; -;  
 DR EMBL: AF248241; AAG31730.1; -;  
 DR EMBL: AF279809; AAF85982.1; -;  
 DR EMBL: AF257080; AAG33126.1; -;  
 DR Genbank: HGNC:6283; KCNK9.  
 DR MIM: 605874; -;  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR003092; TASK\_channel.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR PRINTS: PR0133; 2PORKCHANNEL.  
 DR PRINTS: PR01095; TASKCHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 9 29 POTENTIAL.  
 FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 108 128 POTENTIAL.  
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 159 179 POTENTIAL.  
 FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 219 239 POTENTIAL.

FT DOMAIN 240 374 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 374 AA; 42263 MW; 8A19EAE5A4D7E38 CRC64;  
 Query Match 54.7%; Score 1116; DB 1; Length 374;  
 Best Local Similarity 59.0%; Pred. No. 8.7e-81;  
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;  
 OY 1 MKRONRTIALVCTFYLLVGAADVDALESEBELEROLEROELRLARYLSGGYE 60  
 DB 1 MKRONRTIALVCTFYLLVGAADVDALESEBELEROLEROELRLARYLSGGYE 60  
 OY 61 ELERVYRLPKRAGVQVMPAGSFPAITVITTYGGAHPSTGGKVCMPYALGIP 120  
 DB 61 ELERVYRLPKRAGVQVMPAGSFPAITVITTYGGAHPSTGGKVCMPYALGIP 120  
 OY 61 QLELVLOSPPHAGVQVMPAGSFPAITVITTYGGAHPSTGGKVCMPYALGIP 120  
 DB 61 QLELVLOSPPHAGVQVMPAGSFPAITVITTYGGAHPSTGGKVCMPYALGIP 120  
 OY 121 TLVMPQSLGERINTVLYLLHRRKKGLKRRADVSNANVLYGFEFCISTLCGAAPSH 180  
 DB 121 TLVMPQSLGERINTVLYLLHRRKKGLKRRADVSNANVLYGFEFCISTLCGAAPSH 180  
 OY 121 TLVMPQSLGERINTVLYLLHRRKKGLKRRADVSNANVLYGFEFCISTLCGAAPSH 180  
 DB 121 TLVMPQSLGERINTVLYLLHRRKKGLKRRADVSNANVLYGFEFCISTLCGAAPSH 180  
 OY 181 YEHMTFQAVYVCFITLTITIGFDVVALQKQALQPOVAFSFFYITGLTVIGAFIN 240  
 DB 181 YEHMTFQAVYVCFITLTITIGFDVVALQKQALQPOVAFSFFYITGLTVIGAFIN 240  
 OY 181 CEMSFPMHYVYCFITLTITIGFDVVALQKQALQPOVAFSFFYITGLTVIGAFIN 240  
 DB 181 CEMSFPMHYVYCFITLTITIGFDVVALQKQALQPOVAFSFFYITGLTVIGAFIN 240  
 OY 241 LVVLRPMNAEDKRDALHLLFRNGAGGGGCGSAHTTDTASTAAGCGGRNVY 300  
 DB 241 LVVLRPMNAEDKRDALHLLFRNGAGGGGCGSAHTTDTASTAAGCGGRNVY 300  
 OY 301 -LEVLFQSMQSLWKKSEKQKQISPMIIPRLSDPCVDSHSPPGCGGRVSPTR 359  
 DB 301 -LEVLFQSMQSLWKKSEKQKQISPMIIPRLSDPCVDSHSPPGCGGRVSPTR 359  
 OY 287 KADVPDLSQVSCSTCYRSOD---YGRSAVAPNSFSAKLAPHYFHSIKIEIISPTLK 343  
 DB 287 KADVPDLSQVSCSTCYRSOD---YGRSAVAPNSFSAKLAPHYFHSIKIEIISPTLK 343  
 OY 360 RCLSGAPRSATSVSTGLHSLTFPGLMKRRSSV 394  
 DB 360 RCLSGAPRSATSVSTGLHSLTFPGLMKRRSSV 394  
 OY 344 NSLFP---SPSSISIPGLHSFIDHQRLLMKRRRSV 374  
 DB 344 NSLFP---SPSSISIPGLHSFIDHQRLLMKRRRSV 374  
 RESULT 5  
 C1M9\_CAVPO  
 ID C1M9\_CAVPO STANDARD; PRT; 365 AA.  
 AC 09UL58;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DE Potassium channel subfamily K member 9 (acid-sensitive potassium  
 DE channel protein TASK-3) (TWIK-related acid-sensitive K<sup>+</sup> channel 3).  
 GN KCNK9 OR TASK3.  
 OS Cavia porcellus (guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
 NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20287530; PubMed=10747866;  
 RA Rajan S., Wilschmeyer E., Liu G.X., Prestig-Mueller R., Daut J.,  
 RA Karschin A., Derst C.;  
 RT "TASK-3, a novel tandem pore domain acid-sensitive K<sup>+</sup> channel. An  
 RT extracellular histidine as pH sensor.";  
 RL J. Biol. Chem. 275:16650-16657(2000).  
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
 CC CHANNEL PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
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```

CC -----
DR EMBL: AF212827; AAF63706.1; -
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003092; TASK_channel.
DR Pfam: PF00520; Ion_trans.1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01095; TASKCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 9 29 POTENTIAL.
FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 108 128 POTENTIAL.
FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 179 POTENTIAL.
FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 219 239 POTENTIAL.
FT DOMAIN 240 365 CYTOPLASMIC (POTENTIAL).
FT CARBOHD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 365 AA: 40769 MW: 261DC973EF53AF91 CRC64:

Query Match 52.4%; Score 1069.5; DB 1; Length 365;
Best Local Similarity 57.1%; Pred. No. 3.9e-77;
Matches 226; Conservative 43; Mismatches 94; Indels 33; Gaps 6;

OY 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELROOELRARNYNSGGYE 60
DB 1 MKRONVRLSLIACFTYLLVGAAVFDALSDHEKREBEKKAEEIRIRKYNISTEDYR 60
OY 61 ELERVRLRKPKKGVOMRPAFSEFATVTITIGYAAASTOGKFCMFYALGIPL 120
DB 61 QLEVLIIQSEHRAKGVOMRPAFSEFATVTITIGYAAAGTIDGKAFMFYALGIPL 120
OY 121 TLVNFOSIGERINTLVRYLRLHRAKGLRRADYSMMANVLIIGFSCISTLCIGAAFSH 180
DB 121 TLVNFOSIGERINTLVRYLRLHRAKGLRRADYSMMANVLIIGFSCISTLCIGAAFSH 180
OY 121 TLVNFOSIGERINTLVRYLRLHRAKGLRRADYSMMANVLIIGFSCISTLCIGAAFSH 180
DB 121 TLVNFOSIGERINTLVRYLRLHRAKGLRRADYSMMANVLIIGFSCISTLCIGAAFSH 180
OY 181 YEHTFPQAYYYCFTLTITIGFDYVALQKDALOTQYVAFSVVYLLTGLTYGALN 240
DB 181 CEESFFHAYYYCFTLTITIGFDYVALQKDALOTQYVAFSVVYLLTGLTYGALN 240
OY 241 LVVLRFTMADEKRADEHRLALLTRNGACGGGGGSAHTTDTASTAA--AGCGGRN 298
DB 241 LVVLRFTMADEKRADEHRLALLTRNGACGGGGGSAHTTDTASTAA--AGCGGRN 298
OY 241 LVVLRFTMADEKRADEHRLALLTRNGACGGGGGSAHTTDTASTAA--AGCGGRN 298
DB 241 LVVLRFTMADEKRADEHRLALLTRNGACGGGGGSAHTTDTASTAA--AGCGGRN 298
OY 299 VYAEVLHFQSMCCLWYKSRKLOYSLIPMIIPRLDSTSDTCVEQSHSSPGGGGRYSDPS 358
DB 299 VYAEVLHFQSMCCLWYKSRKLOYSLIPMIIPRLDSTSDTCVEQSHSSPGGGGRYSDPS 358
OY 292 -----DLQSVSCACYSRSP--ONFGATLAPQPLHSISCRIEET-----SPS 331
DB 292 -----DLQSVSCACYSRSP--ONFGATLAPQPLHSISCRIEET-----SPS 331
OY 359 RRCLOSGAPRSAISSVSGHLSLSTRFLMKRRSY 394
DB 359 RRCLOSGAPRSAISSVSGHLSLSTRFLMKRRSY 394
OY 332 --TLKNSLFPSPISISSVGLHSGFDNRLMLRKRSY 365
DB 332 --TLKNSLFPSPISISSVGLHSGFDNRLMLRKRSY 365

RESULT 6
C1W2_MOUSE STANDARD: PRT. 411 AA.
AC P97438;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium
DE channel protein TREK-1) (two-pore potassium channel 1PKC1) (TREK-1 K+
DE channel subunit).
DE KCNK2.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.

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RC TISSUE=Brain;
RX MEDLINE=97157476; PubMed=9003761;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RT "Cloning, functional expression and brain localization of a novel
RT uncoupled, outward-rectifier K+ channel.";
RL EMBL J. 15:6854-6862(1996);
RM [2]
RP REVISIONS.
RC TISSUE=Brain;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RP [3]
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC HIPPOCAMPUS AND CEREBELLUM.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U73488; AAC53005.2; -.
DR MGD: MGI:109366; Kcnk2.
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003976; Trek_channel.
DR Pfam: PF00520; Ion_trans.1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01499; TREKCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 POTENTIAL.
FT DOMAIN 129 155 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 157 177 POTENTIAL.
FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 228 POTENTIAL.
FT DOMAIN 238 268 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 273 293 POTENTIAL.
FT DOMAIN 294 411 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT SENSITIVITY.
FT DOMAIN 354 411 REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT CARBOHD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHD 119 119 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 411 AA: 45297 MW: 8F976DD103EFA05 CRC64:

Query Match 18.1%; Score 370; DB 1; Length 411;
Best Local Similarity 28.0%; Pred. No. 5.8e-22;
Matches 109; Conservative 66; Mismatches 126; Indels 88; Gaps 13;

OY 1 MKRONVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELROOELRARNYNSGGYE 60

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Db 42 MKKRTVSTFLVY--VLYLIGAAVKALEQPOEISQRTTIVIOKOTFLAQAHCVNS--T 97
OY 61 ELERVVLR-L-KPKKAV-----QMRFGSPYPAITVTTTGGHAAPSTGGKV 108
Db 98 ELDELQOIVAAINAGIIFPLGNSSNOVSHMDLGSFFFGVITTTGGFNGISPRTEGKI 157
OY 109 FCMFVALLGIPPLTVAFOSIGERINTLVRYLLHRAKKGGMRRAD-----VSM 156
Db 158 FCIIVALLGIPLEGFLAGVGDLGITF-----GNGIAVEDTFLKMNVSQTKIRI 208
OY 157 ANKVLIGFSCISTLCIGAAASHYEHMTFFQAYVYCFITLTITGGDYVALOKDALOT 216
Db 209 ISTIIFILGCVLFVLPVAFIEFKHIGMSALDAIYFVITLTITGGDYVAGGSD--IEY 266
OY 217 QPOYVAFSVYILITGLTVIGAFNLVY--VLRFTMAAEDEKRDRAHRAALLTRNGAGGGG 274
Db 267 LDFYKRVVFWFLLVGLAFVAAVLSMIGDMLRVYSKTKTEV-----307
OY 275 GGGSAHTTDTASTAAAGGGFRNVYAENVLHFSQMSCLWYKSREKLOYSPMIIIPDLS 334
Db 308 GEFRMAAAEWTA-----NYTAE-----FKETRRRLSVEL-----YDKF 340
OY 335 TSDTCVGEQSHSPGCGGRYS-D-TPSRCL 362
Db 341 QRATSVKRLISAEIAGNHNQELTPCRRTL 369

RESULT 7
CIV2_HUMAN STANDARD; PRT; 426 AA.
ID CIV2_HUMAN 09JUN93;
AC 095069;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel TREK-1) (TREK-1 K+ channel subunit) (Two-pore potassium channel TRPK1).
DE KCNK2 OR TREK1 OR TREK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9254548; Pubmed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";
RL Nat. Neurosci. 2:422-426(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RL Submitted (MAR-1997) to the EMBL/Genbank/DBS databases.
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
CC -----
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CC -----
DR EMBL: AF129399; AAD47569.1; -
DR EMBL: AF004711; AAD01203.1; -

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DR Genew; HGNC:6277; KCNK2.
DR MIM; 603219; -.
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003976; Trek_channel.
DR Pfam: PF00520; Ion_trans_1.
DR PRINTS: PR01333; 2PORECHANNEL.
DR PRINTS: PR01499; TREKCHANNEL.
DR Tonic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.
KW DOMAINS
FT 1 61 CYTOPLASMIC (POTENTIAL).
FT 2 82 POTENTIAL.
FT 3 144 PORE-FORMING 1 (POTENTIAL).
FT 4 172 POTENTIAL.
FT 5 192 CYTOPLASMIC (POTENTIAL).
FT 6 223 POTENTIAL.
FT 7 224 PORE-FORMING 2 (POTENTIAL).
FT 8 283 POTENTIAL.
FT 9 308 CYTOPLASMIC (POTENTIAL).
FT 10 309 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY (BY SIMILARITY).
FT 11 378 REQUIRED FOR BASAL CHANNEL ACTIVITY (BY SIMILARITY).
FT 12 426 N-LINKED (GLCNAC. .) (POTENTIAL).
FT 13 426 N-LINKED (GLCNAC. .) (POTENTIAL).
FT 14 426 MISSING (IN REF. 2).
FT 15 426 RLV -> DMV (IN REF. 2).
FT 16 426 S -> N (IN REF. 2).
FT 17 426 A -> T (IN REF. 2).
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Rx MEDLINE=20435789; PubMed=10860510;
RA Lesage F., Terrenoire C., Romey G., Ladusnski M.;
RT "Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple
RT regulations by polyunsaturated fatty acids, lysophospholipids and Gs,
RT G1, and Gq protein-coupled receptors.";
RL J. Biol. Chem. 275:28398-28405 (2000).
CC -1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
CC ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING
CC UNSATURATED FREE FATTY ACIDS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PANCREAS AND KIDNEY
CC AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see license@sib-sib.ch)."
CC -----
DR EMBL; AF279890; AACG151.1; -
DR Genew; HGNC:6273; KCNK10.
DR MIM; 605873; -
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000636; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein..
FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 72 92 POTENTIAL.
FT TRANSMEM 154 180 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 182 202 POTENTIAL.
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 254 POTENTIAL.
FT TRANSMEM 263 294 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 299 319 POTENTIAL.
FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 538 AA; 57664 MW; 8BA615B08D147FBC CRC64;
Query Match 17.1%; Score 349.5; DB 1; Length 538;
Best Local Similarity 32.8%; Pred. No. 3.2e-20;
Matches 95; Conservative 53; Mismatches 109; Indels 33; Gaps 10;
QY 1 MKRONVRLTALIVCTFTYLGVGAVFADLSEPELIERORLEKROOE-LRAYNLSDGQY 59
Db 67 MKKMTV--VAIFVYVVYVLVGLVFRALDEPFESSQKNTALEKAELRLRHVCVSP-- 121
QY 60 EELERVVLR-LKPKAGV-----QMRFAGSEFYATVYTTTIGYGHAAPSTDGK 107
Db 122 QELFTLLIOHADADNAGVSPIGNSSNNSSHHDLDSAPFAGTAVTTTIGYGIADSTEGK 181
QY 108 VECFAYMLLGLPLVLVWFSIGERINLVRLLHRAKKGGLGMRADVSMAM-----VLI 162
Db 182 IFCFLVAFIPIGLPLGFLAGIGDGLTIGKSIARVEK--VERKKVVSQTRIRVISTLTF 239
QY 163 GFSPSCISLTLCIGAAAFSHYEHMTFFQAAVYCYFILTITGGFDYVALQKDAQLQTOPQYVA 222
Db 240 ILACCIYFVTIPAVIKFYIEBWTALSTIYFVVLITTYGDFDVA--GGMADINRWKIP 298
QY 223 FSEFYILTGLTVIGAFNLV--VLRPMTMADEKRD-----AEHRLALT 265
Db 299 LVWFWIILVGLAVFAAVILSMIGDWIRVLSKRTKEVGGELKAHAIAEMKANVT 348

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ID	C1WA_RAT	STANDARD:	PRT:	538 AA.
RESULT 9				
AC	Q9J54:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).			
GN	CKNK10 OR TREK2.			
OC	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20298807; PubMed=10747911;			
RA	Bang H., Kim Y., Kim D.;			
RT	"TREK-2", a new member of the mechanosensitive tandem-pore K+ channel family.";			
RL	J. Biol. Chem. 275:17412-17419 (2000).			
CC	- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS. ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING UNSATURATED FREE FATTY ACIDS.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN, AND TESTIS.			
CC	- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; AF196965; AAF75132.1;			
DR	InterPro: IPR003280; K+channel_2pore.			
DR	InterPro: IPR001622; K+channel_pore.			
DR	InterPro: IPR000636; M+channel_nlg.			
DR	InterPro: IPR003976; Trek_channel.			
DR	Pfam; PF00520; Ion_trans_1.			
DR	PRINTS; PRO1333; 2PORECHANNEL.			
DR	PRINTS; PRO1499; TREKCHANNEL.			
KW	ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.			
KW	-----			
FT	DOMAIN 1 71			
FT	TRANSMEM 92			
FT	DOMAIN 154 180			
FT	TRANSMEM 182 202			
FT	DOMAIN 203 233			
FT	TRANSMEM 234 254			
FT	DOMAIN 263 294			
FT	TRANSMEM 299 319			
FT	DOMAIN 320 338			
FT	CARBOHD 144 144			
FT	CARBOHD 147 147			
SO	SEQUENCE 538 AA; 59800 MW; 1FF33F0AA52B97E4 CRC64;			
Query Match	17.1%; Score 349.5; DB 1; Length 538;			
Best Local Similarity	32.8%; Pred. No. 3.2e-20;			
Matches	95; Conservative 53; Mismatches 109; Indels 33; Gaps 10;			
QY	1 MKRONFTALIVCTFTLLVGAALVDALESEPELIERORLELROQE-LRARIYLSQGGY 59			
DB	67 MKWTV--VAIFVVVVVYLVTGLVFRALDEPFSSQKNTALKEAEFLRHICVSP--- 121			
QY	60 ELERVYLVR-LAKPKAGV-----QKRFAGSFYFATVITTTTGIGYGAAPSTGGK 107			
DB	122 QELTLLTDLHADADNAGVSPVGNSSNSSSSHHDLGSAFFACTVITTTTGIGYGAAPSTGGK 181			



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Oy      108 VECMEVATLGLPIPLVTMVSQSGERINTLVRYLTHRAKCKLGRADSVMAN-----VLI 166
Db      182 IFCLIALAFGLPFPFELLAGIGDQDGLTIFGKSIAYEK--YRRKQVSOQTKRIVSTILF 239
Oy      163 GFPSICSTFLCIGAAAFSHYEHWTFEQAAYYCITLTITIGFGDYALQKDAQLOTOPQYVA 222
Db      240 ILACIIVEVTPITPAVIFKYLEGWTALESIYFVVVLTLYVGDFEVA--GAGNAINRYEMXP 298
Oy      223 FSYVYIITGLVIGAFNLV--VLRFMTNMADEKRD-----AERALLT 265
Db      299 LVMEVITVLGLVFAVILSMIDMLRVLSKTRKEVEGEIKAHAAEKWANTV 348

RESULT 10
C1M4_HUMAN          STANDARD:      PRT:      393 AA.
AC      Q9NVG8:
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
DE      stimulated potassium channel protein) (TRAAK).
GN      KCNK4 OR TRAAK.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX      NCBI_TaxID=9606;
[1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=20499203; PubMed=11042359;
RA      Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
RA      Kelsell R.E., Murdoch P.R., Randall A.D., Rennie G.I., Gloger I.S.,
RT      "Cloning, localisation and functional expression of a novel human;
RT      cerebellum specific, two pore domain potassium channel.";
RL      Brain Res. Mol. Brain Res. 82:74-83(2000).
[2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Frontal cortex;
RA      Gray A.T.;
RT      "Assignment of KCNK4 encoding the human potassium channel TRAAK to
RT      chromosome 11.";
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20231699; PubMed=10767409;
RA      Lesage F., Malngret F., Lazdunski M.;
RT      "Cloning and expression of human TRAAK, a polyunsaturated fatty
RT      acids-activated and mechano-insensitive K(+) channel.";
RL      FEBS Lett. 471:137-140(2000).
-1-  FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC      POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC      EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
CC      -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC      -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC      CHANNELS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation.
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CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@sdb.ch).
CC      -----
DR      EMBL; AF248242; AAC31731.1; -
DR      EMBL; AF247042; AAF64062.1; ALT_INIT.
DR      Genew: HGNC:6279; KCNK4.
DR      MIM: 605720; -
DR      InterPro: IPR003280; K+channel_2pore.
DR      InterPro: IPR001622; K+channel_pore.

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Query	Match	Similarity	Score	DB	Length
Best Local	Similarity	31.0%	Pred. No. 8.5e-19;		
Matches	Conservative	43;	Mismatches	112;	Indels 63; Gaps 8;
DR	InterPro: IPR000336; M+channel_nlg.				
DR	Pfam: PF00520; Ion_trans. 1.				
DR	PRINTS: PR01333; 2PORKCHANNEL.				
KW	Ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein.				
KW	DOMAIN	1	3	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	4	24	POTENTIAL.	
FT	DOMAIN	89	113	PORE-FORMING 1 (POTENTIAL).	
FT	TRANSSEM	118	138	POTENTIAL.	
FT	DOMAIN	140	171	CYTOPLASMIC (POTENTIAL).	
FT	TRANSSEM	172	192	POTENTIAL.	
FT	DOMAIN	197	221	PORE-FORMING 2 (POTENTIAL).	
FT	TRANSSEM	234	254	POTENTIAL.	
FT	DOMAIN	255	393	CYTOPLASMIC (POTENTIAL).	
FT	CARBOHYD	78	78	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	82	82	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CONFLICT	328	328	P -> L (IN REF. 2).	
SO	SEQUENCE	393 AA;	42704 MW;	7F1B853A0A9AD57D CRC64;	
Query Match	Similarity	16.1%;	Score	329.5;	DB 1;
Best Local	Similarity	31.0%;	Pred. No. 8.5e-19;		
Matches	Conservative	43;	Mismatches	112;	Indels 63; Gaps 8;
QY	9 LALLVCFITLLVGAAPFDALSESE-LEIQRLELRQQLRARKYNLSQ-----	56			
DB	7 LALLVALLVLLVSGALVFRALEQPHQOAELEVERKELRAHPCVSDOELGLIKEVA	66			
QY	57 ---GGEYELERHVRLPKHKGAVOMREFSGFYFAITVTTTIGYGAAPSTDGKVCMFY	113			
DB	67 DALGGADPEINISNSNSHSA---WDGSAFFSGITITTTIGYGNVALRTDAGRLFCIFY	123			
QY	114 ALDCIPLTVFQSLGERINTLVRYLLHRAKKGJGMRAD-----YSMANVLLIG	163			
DB	124 ALVGIPIFGILLACVGRIGSGSLRH-----GIGHLEAIFLKHVPEELRVLSAMLEL	176			
QY	164 FFGSISTLCIGAAAFSHYEHMTFFQAYYCITLTITIGFGDYVALQDQALQTPQYVAF	223			
DB	177 LIGCLLVLPVTFPFYFCWEDMSKELAIYFVTLITVGFQYVAGADR--QDSPATQPL	234			
QY	224 SFVYILTG-----LTVIGAFNLVYLRFMTMAAEDEKRDAREHALLTRNGAGGGGGG	276			
DB	235 VMFVILLGLAFASVLTITIGWMLRVSVR-----TRAEMGGLRAQA	275			
QY	277 GSAHTTDTASTAAG 292				
DB	276 ASWTGTVTARYTORAG 291				
RESULT 11					
CITM_MOUSE					
ID	CITM_MOUSE	STANDARD:	PRT:	398 AA.	
AC	088454;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-stimulated potassium channel protein) (TRAK).				
GN	KCNK4 OR TRAK.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID:10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=98292450; PubMed=9628867;				
RA	Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M., Lazdunski M.;				
RT	"A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids."				
RL	EMBO J. 17:3297-3308(1998).				
RN	[2]				
RP	ACTIVATION.				



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RX MEDLINE-99254548; PubMed-10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels."
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC EXTERNAL K+ CONCENTRATIONS.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND
CC 2/TRUNK/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
CC DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
CC TESTIS.
CC -1- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
CC FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANESTHETICS SUCH AS
CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF056492; AAC40181.1; -
DR MGD; MGI:1298234; Kcnk4.
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01333; 2PORECHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein; Alternative splicing.
FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 4 24 PORE-FORMING 1 (POTENTIAL).
FT DOMAIN 89 113 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 119 139 POTENTIAL.
FT DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 198 222 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 235 255 POTENTIAL.
FT DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 63 67 KLVAE -> KAMAI (IN ISOFORM 2).
FT VARSPLIC 68 398 MISSING (IN ISOFORM 2).
SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7AC92 CRC64;

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Query Match 16.0%; Score 326.5; DB 1; Length 398;
Best Local Similarity 31.5%; Pred. No. 1.5e-18;
Matches 85; Conservative 45; Mismatches 95; Indels 45; Gaps 7;

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OY 9 LALVCTFTLLVGAAYDALESEPELIERQRL-ROELRARNLSGGYEELRYVL 67
DB 7 LALLALVLLVLSGALVFOLEQPKMDGRQFDRDHCVSOKSLDEPIKILV 66
OY 68 RLKPKKAGVQ-----WRPAGSFYATVITITIGYGHAPSTDGKVFCEFYAL 115
DB 67 EALGGANPETSMTSSNHSNWSNAGSAFFSGITITITIGYGHAPSTDGKVFCEFYAL 126
OY 116 LGIPITLVFQSLGERINTVLYLLHRAKKGIMRA-----DVSMANWVLI 162
DB 127 VGIPFGMLAGVGRGLSSLR-----RGIGITEAIFLKWHPGGLVRSLSAVLFILI 179
OY 163 GFPSGISLTCIGAAAFSHYHMTFFQAYCYFITLTITIGFDYVALQDQALQTPQY-- 220
DB 180 G---CLFVLTPFVEFYSMESMSKLAIFYIVLTITVGFQDYV--PDGTGQNSPAYOP 234

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OY 221 -----VAFSFYILTGTVIGAFNLVYL 245
DB 235 LWFEWILFGLAFYASVLTITNMRLAVSRR 264

RESULT 12
ID CIVIL_HUMAN STANDARD; PRT; 336 AA.
AC 000180; Q13307;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 1 (inward rectifying potassium
DE channel protein TWIK-1) (Potassium channel KCNO1).
CN KCNK1 OR TWIK1 OR HOH01 OR KCNO1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
RC TISSUE-Kidney;
RX MEDLINE-96183184; PubMed-8605869;
RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,
RA Barhanin J.;
RT "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a
RT novel structure."
RL EMBL J. 15:1004-1014(1998).
RN [2]
RP SEQUENCE FROM N.A., AND REVIEW.
RC TISSUE-Brain;
RX MEDLINE-98122696; PubMed-9462864;
RA Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;
RT "Sequence and function of the two P domain potassium channels:
RT implications of an emerging superfamily."
RL J. Mol. Med. 76:13-20(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-98026667; PubMed-9362344;
RA Orías M., Velazquez H., Tung F., Lee G., Desir G.V.;
RT "Cloning and localization of a double-pore K channel, KCNK1: exclusive
RT expression in distal nephron segments."
RL Am. J. Physiol. 273:F663-F666(1997).
CC -1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND
CC BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
CC -1- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND
CC INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
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CC -----
DR EMBL; U33632; AAB01688.1; -
DR EMBL; U76996; AAB97878.1; -
DR EMBL; U90065; AAB51147.1; -
DR Gene; HGNC:6272; KCNK1.
DR MIM; 601745; -
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR001779; TWIK1_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01096; TWIK1CHANNEL.

```

KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 21 41 POTENTIAL.  
 FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 133 153 POTENTIAL.  
 FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 178 198 POTENTIAL.  
 FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 247 267 POTENTIAL.  
 FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT MOTAGEN 161 T->A: NO EFFECT ON CHANNEL ACTIVITY.  
 SQ SEQUENCE 336 AA; 38143 MW; 2A41D9501323215D CRC64;  
 Query Match 15.7%; Score 320.5; DB 1; Length 336;  
 Best Local Similarity 32.4%; Pred. No. 3,6e-18;  
 Matches 90; Conservative 47; Mismatches 102; Indels 39; Gaps 9;  
 QY 11 LVCTFTYLLVGAVALDALESEBELIERQL-ELRQOELRARNYLSQGYEELERYVLR 69  
 DB 26 LVGLYLLVFGAVVSVSELPEDLLRQELRKRRLFEHCLSEQOLEGFLGRVLEA 85  
 QY 70 KPHKAGV-----QMRAGSYFAITYITTYIGYGHAPSTDGKVFQCFYALLGIPLT 121  
 DB 86 SMGVSVLSNAGSNMMDTSTALFFASTVLTGTGHTVPLSGKGAFCIIYSVIGIPPT 145  
 QY 122 LVWFOSLGERINTLVYLLHRAKGL-----GMRADVSMANVLLGFSCISTLCIG 174  
 DB 146 LELFTRAVVGRIT-----VHVRRLVLYFHIRMGSKOVAYIAVHVLGFLVYSCFFPI 199  
 QY 175 AAASFHYE-HWFFQAYVYCFITLTITGFGDYVA---LQKDALOTOPQYVAFSEFVYL 229  
 DB 200 AAVFSELEDNMNELESFPCFISLSTIGLDYVPGEGYNQKREL-----YKIGTCYLL 254  
 QY 230 TG---LTVIGAFPLNVL---RFMTMNAEDKRDMEH 260  
 DB 255 LGLIAMLVYLETFCLEHLKFRKMFYKKDKDEQVH 292  
 RESULT 13  
 C1W5 HUMAN STANDARD; PRT; 499 AA.  
 AC 095279;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily K member 5 (acid-sensitive potassium channel protein TASK-2) (Twik-related acid-sensitive K+ channel 2).  
 GN KCNK5 OR TASK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE=9903043; PubMed=9812978;  
 RA Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Fauran N.,  
 RA Lazdunski M.;  
 RT Cloning and expression of a novel pH-sensitive two pore domain K+  
 RT channel from human kidney.  
 RL J. Biol. Chem. 273:30863-30869(1998).  
 CC -1- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING  
 CC POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL  
 CC K+ CONCENTRATIONS.  
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED  
 CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION  
 CC IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT  
 CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.  
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, QUININDINE AND EXTERNAL

CC ACIDIFICATION.  
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
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 CC -----  
 CC EMBL: AF084830; AAC79458.1; .  
 CC Genbank: HGNC:6280; KCNK5.  
 CC MIM: 603493; .  
 CC InterPro: IPR003280; K+channel\_2pore.  
 CC InterPro: IPR001622; K+channel\_pore.  
 CC InterPro: IPR000636; M+channel\_nlg.  
 CC Pfam: PF00520; Ion\_trans; 1.  
 CC PRINTS: PR01333; 2PORECHANNEL.  
 CC Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 7  
 FT TRANSMEM 8 26 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 85 112 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 113 133 POTENTIAL.  
 FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 158 180 POTENTIAL.  
 FT DOMAIN 190 215 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 230 250 POTENTIAL.  
 FT CARBOHYD 251 325 CYTOPLASMIC (POTENTIAL).  
 FT MOTAGEN 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 499 AA; 55130 MW; E871A7A4823DA00 CRC64;  
 Query Match 15.6%; Score 319; DB 1; Length 499;  
 Best Local Similarity 32.8%; Pred. No. 7,5e-18;  
 Matches 84; Conservative 47; Mismatches 97; Indels 28; Gaps 8;  
 QY 18 YLVGAVALDALESEBELIE-----RQRLERQOELRARNYLSQGYEELERVV----- 66  
 DB 15 YLVGAVALDALESEBELIE-----RQRLERQOELRARNYLSQGYEELERVV----- 66  
 QY 67 --LRKPKHAKGVOMRAGSYFAITYITTYIGYGHAPSTDGKVFQCFYALLGIPLTLM 124  
 DB 70 OGVAITGNQTFNMNMNPMIFAATVITTYIGYGHAPSTDGKVFQCFYALLGIPLTLM 129  
 QY 125 FOSLGE---RINTLVRYLLHRAKGLGMRADVSMANVLLGFSCISTLCIGAAAFSH 180  
 DB 130 ISALGKFFGGRKRLGQFL---TKRGVSLRKAQITCTVIFV--KGVHVLVIPPVRYV 184  
 QY 181 YEHWFQAYVYCFITLTITGFGDYVALQKDALOTOPQYVAFSEFVYLLTGLVIGAFPLN 240  
 DB 185 TEGMNYIEGLYSEFISLSTIGLDYVPGEGYNQKREL-----YKIGTCYLL 254  
 QY 241 LVYLRFTMNAEDK 256  
 DB 244 MKVSMFEVHKAIKKR 259  
 RESULT 14  
 C1W1 MOUSE STANDARD; PRT; 336 AA.  
 AC 008581;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily K member 1 (inward rectifying potassium channel protein TWIK-1).  
 GN KCNK1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain:
RX MEDLINE=97165959; PubMed=90138552;
RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
RA Lazdunski M.;
RT "The structure, function and distribution of the mouse TWIK-1 K+
RT channel.";
RL FEBS Lett. 402:28-32(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RX MEDLINE=98218573; PubMed=9559671;
RA Arrighi I., Lesage F., Solmeica J.-C., Carle G.F., Barhanin J.;
RT "Structure, chromosome localization, and tissue distribution of the
RT mouse twik K+ channel gene.";
RL FEBS Lett. 425:310-316(1998).
CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,
CC KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
CC EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM, MODERATE
CC EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
CC OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
CC MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
CC CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
CC CORTEX.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
CC STABILIZES AFTER DAY 8.
CC -1- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
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CC -----
DR EMBL; AF033017; AAC16973.1; -.
DR MGD; MGI:109322; Kcnk1.
DR InterPro: IPR003280; K+-channel_2pore-.
DR InterPro: IPR001622; K+-channel_pore.
DR InterPro: IPR000635; M+-channel_nlg.
DR InterPro: IPR001779; TWIK1_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01096; TWIK1CHANNEL.
DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
DR Glycoprotein.
FW DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 21 41 POTENTIAL.
FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).
FT TRANSSEM 133 153 POTENTIAL.
FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 178 198 POTENTIAL.
FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).
FT TRANSSEM 247 267 POTENTIAL.
FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 336 AA; 38275 MW; A596060A18266FD4 CRC64;
Query Match 15.6%; Score 318.5; DB 1; Length 336;
Best Local Similarity 32.4%; Pred. No. 5,2e-18;
Matches 90; Conservative 46; Mismatches 103; Indels 39; Gaps 9;
11 LIVCTFTYLLVGAAPDALESEPELIERQRL-ELRQOELRARNYLSGGYEELERVYRL 69
::: ||| ||| ||| : : : ||| ||| ||| : : : ||| : : : ||| : : : |||

```

Db	26	LVIGVLLYLVFGAVVSSSELPEDDLRQLRLKLRLEEHCECSSEQLQPLGRVLEA	85
Qy	70	KPKHAGY-----QWRPAGSFYEATVITTTIGTGAAPSTDGKFCMFYALLGIPLT	123
Db	86	SNVGSVLSNASGNNMMMDFTSALFFASVLTSTTGGHVFPLSDGGKACFIISYIGIPFT	145
Qy	122	LWNFQSLGGINLNLVYVLLHRRKKGL-----GMRADVSANNVLLGFSCSLTLCIG	174
Db	146	LLFLTALVAVKQVT-----VAVRRRPVLYRHIMWGSFVKOVVALVHVVLLGFVTVCSEFPIT	199
Qy	175	AAAFSHSE-ITWTEFFQAYVYCCITLITIGDGYVA-----LQKDALQTOPOYVAESFYIL	228
Db	200	AAAFSVLEEDMNNLFESFVFCFISLSTIGLGDVYPPGEGINQKREL-----IKIGITCVLL	254
Qy	230	TG---LTVIGAFNLVVL---RFMTMADEKRDAAEH	260
Db	255	IGITMLVLYETFCELHKKFKRMKYVKKDDLDVH	292
RESULT 15			
Clw6	HUMAN	STANDARD:	PRT: 313 AA.
AC	09Y257: 09HB47:		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Potassium channel subfamily K member 6 (inward rectifying potassium channel protein TWIK-2) (TWIK-originated similarity sequence).		
DE	KCNK6 OR TWIK2 OR TOSS.		
GN	KCNK6 OR TWIK2 OR TOSS.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID:9606;		
NI	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE-Testis:		
RX	MEDLINE=99285568; PubMed=10359073;		
RA	Pountney D.J., Gulkaiov I., Vega-Saenz de Miera E., Holmes D.,		
RT	Saganich M., Rudy B., Artman M., Coetzee W.A.;		
RT	"Identification and cloning of TWIK-originated similarity sequence (TOSS): a novel human 2-pore K <sup>+</sup> channel principal subunit."		
RL	FEMS Lett. 450:191-196(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF CYS-53.		
RC	TISSUE-Brain:		
RX	MEDLINE=99175162; PubMed=10075682;		
RA	Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,		
RT	Melita Y., Forsythe J.R., Yost C.S.;		
RT	"TWIK-2, a new weak inward rectifying member of the tandem pore domain potassium channel family."		
RL	J. Biol. Chem. 274:7887-7892(1999).		
RN	[3]		
RP	ERRATUM.		
RA	Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,		
RT	Melita Y., Forsythe J.R., Yost C.S.;		
RL	J. Biol. Chem. 274:24440-24440(1999).		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.		
RX	MEDLINE=20435832; PubMed=10867187;		
RA	Patel A.J., Malingret F., Magnone V., Fosset M., Lazdunski M.,		
RT	Honore E.;		
RT	"TWIK-2, an inactivating 2P domain K <sup>+</sup> channel."		
RL	J. Biol. Chem. 275:28722-28730(2000).		
RN	[5]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE-Pancreas:		
RA	Strassberg R.;		
RL	Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.		
CC	-1- FUNCTION: Exhibits outward rectification in a physiological K(+) gradient and mild inward rectification in symmetrical K(+) conditions.		
CC	-1- SUBUNIT: HOMODIMER (POTENTIAL).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).		

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are  
CC produced by alternative splicing.  
CC -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES  
CC TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN  
CC PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED  
CC IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.  
CC -1- LOWEST EXPRESSION DETECTED IN BRAIN.  
CC -1- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL  
CC DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARIUM.  
CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
CC CHANNELS.  
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CC -----  
DR EMBL: AF134149; AAD22980.1; -  
DR EMBL: AF117708; AAD24000.1; -  
DR EMBL: AF281302; AAG10506.1; -  
DR EMBL: AF281303; AAG10507.1; -  
DR EMBL: BC004367; AAH04367.1; -  
DR GeneW: HGNC:6281; KCNK6.  
DR MIM: 603939; -  
DR InterPro: IPR001632; K+channel\_pore.  
DR InterPro: IPR000636; M+channel\_nlg.  
DR InterPro: IPR001779; TWIK1\_channel.  
DR Pfam: PF00520; Ion\_trans; 1.  
DR PRINTS: PR01096; TWIK1CHANNEL.  
KM Ionic channel; Transmembrane; Ion transport; Potassium transport;  
KW Glycoprotein; Alternative splicing.  
FT DOMAIN 1 4  
FT TRANSMEM 5 25 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 90 115 PORE-FORMING 1 (POTENTIAL).  
FT TRANSMEM 121 141 POTENTIAL.  
FT DOMAIN 142 172 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 173 193 POTENTIAL.  
FT DOMAIN 199 223 PORE-FORMING 2 (POTENTIAL).  
FT TRANSMEM 236 256 POTENTIAL.  
FT DOMAIN 257 313 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 1 134 MISSING (IN ISOFORM 2).  
FT MUTAGEN 53 53 C->A: NO CHANNEL ACTIVITY.  
SQ SEQUENCE 313 AA; 33747 MW; 1379382DFB0575DE CRC64;  
  
Query Match 14.5%; Score 295.5; DB 1; Length 313;  
Best Local Similarity 31.7%; Pred. No. 3.1e-16;  
Matches 90; Conservative 40; Mismatches 95; Indels 59; Gaps 12;  
  
QY 18 YLVGAAVDALESEPELIERORLEKQOELNARYN-----LSOGGYEELE 63  
DB YLVGGLLVARLEGPHEARLELRALQLQSPCAVAPALDAFVERVLAAG--RLG 73  
QY 64 RVLRLKPKHAGVQ--WRPAGSEFAIVITTTIGGHAAPSTDGKVCMEYALLGIP 120  
DB RVLNANAGSANNADPAMPDFASLFPASTLTITTVGGYTPPLDAGKAFSIAFALGVPT 133  
QY 121 TLVMEQSLGERINTLVRYLLHRAKKIGM-----RRADVSMANWVLIGFSCISITLC-- 172  
DB TLVLLTASQRLSL--LTHVPLSLSRMGMDPRRA-----ACMHLVALLGVVTVYVCF 186  
QY 173 IGAAPAFSHYH-WTFPQATYYCFITLTITGGFDYVALQKDALQTOPQ--YVASEFYI 228  
DB VPAVIFAHLEAMSFDAFYCFISLTGLDYPGE---APGQPYRALYKVLVTVYVL 242  
QY 229 LTGLT-----VIGAFNLVYLRMT-----MNAEDEKR 256  
DB FLGLVAMVVLQTFRRHVSDLHGCTELILPPCPASFNDEDDR 286

Search completed: July 1, 2003, 15:16:07  
Job time : 25 secs



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DB 42 EIERVYLRKPKHAGVQWRFAGSFYFAITVITIGYGHAPSTDGCKVFCMFYALGIPL 101
OY 121 TLMFOSLGERINTLVRYLLHRAKRGIGRRADVANNVLTGFESCISTLCIGAAAFSH 180
DB 102 TLMFOSLGERINTLVRYLLHRAKRGIGRRADVANNVLTGFESCISTLCIGAAAFST 161
OY 181 YEHMFEFOAYYYCFTLTITIGFDYVALQKDALQTOPQYVAFSYIITGLTIGAFILN 240
DB 162 YEHMFEFOAYYYCFTLTITIGFDYVALQKDALQTOPQYVAFSYIITGLTIGAFILN 221
OY 241 LVYLRMTNNAEDEKDAEHRALLTRNGOAGGGG-----GGSAAHTTDRASSTAA- 291
DB 222 LVYLRMTNNAEDEKDAEHRALLTRNGOAGGGG-----GGSAAHTTDRASSTAA- 281
OY 292 -----GGGFRNRYAEVLHFOQSMCCLMYKSRKLOYSIPMITPRDISTSDCVEOS 343
DB 282 GAGVGVGSGSFRNRYAEVLHFOQSMCCLMYKSRKLOYSIPMITPRDISTSDCVEOS 341
OY 344 HSSPGGGRYSDTPSRRLCSGAPRSATSVSTGLSLSTFRGLMKRRSSV 394
DB 342 HSSPGGGRYSDTPSRRLCSGAPRSATSVSTGLSLSTFRGLMKRRSSV 392

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## RESULT 2

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OY 090X34 PRELIMINARY; PRT; 299 AA.
AC 090X34:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative potassium channel DP4 (Fragment).
GN KCNK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA Kaczmarek L.K.;
RU Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DB EMBL; AB022821; AAD09338.1; -.
DR MGD; MGI:1100509; Kcnk3.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000636; M+channel_nlg.
DR InterPro; IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PRO1584; 2PORKCHANNEL.
DR PRINTS; PRO1584; TASKCHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KW Ionic channel.
FT NON_TER 1
FT TER 299
SQ SEQUENCE 299 AA; 33325 MW; DCD41DBA212939C4 CRC64;

```

Query Match 65.3%; Score 1333; DB 11; Length 299;  
 Best Local Similarity 88.9%; Pred. No. 2.5e-116;  
 Matches 263; Conservative 7; Mismatches 18; Indels 8; Gaps 1;

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OY 4 QNVRTLALIVCFYLLVGAAVFDALSEPELIERORLELROELRARRYLSQGYEEL 63
DB 2 ENVRTLALIVCFYLLVGAAVFDALSEPELIERORLELROELRARRYLSQGYEEL 61
OY 64 RYVLRKPKHAGVQWRFAGSFYFAITVITIGYGHAPSTDGCKVFCMFYALGIPLTV 123
DB 62 RYVLRKPKHAGVQWRFAGSFYFAITVITIGYGHAPSTDGCKVFCMFYALGIPLTV 121
OY 124 MFOSLGERINTLVRYLLHRAKRGIGRRADVANNVLTGFESCISTLCIGAAAFSHYEH 183
DB 122 MFOSLGERINTLVRYLLHRAKRGIGRRADVANNVLTGFESCISTLCIGAAAFSYER 181

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OY 184 WFEFOAYYYCFTLTITIGFDYVALQKDALQTOPQYVAFSYIITGLTIGAFILN 243
DB 182 WFEFOAYYYCFTLTITIGFDYVALQKDALQTOPQYVAFSYIITGLTIGAFILN 241
OY 244 LRFMTNNAEDEKDAEHRALLTRNGOAGGGG-----GGSAAHTTDRASSTAA 291
DB 242 LRFMTNNAEDEKDAEHRALLTRNGOAGGGG-----GGSAAHTTDRASSTAA 297

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## RESULT 3

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OY 09ESM4 PRELIMINARY; PRT; 301 AA.
AC 09ESM4:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE TWIK-related acid-sensitive K+ channel splice variant (TASK1c).
GN KCNK3c.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohya S., Kitsuawa M., Imaizumi Y.;
RA TISSUE=AOIRA;
RT "TWIK-related acid-sensitive K+ channel (TASK1) (KCNK3) splice
RT variant";
RU Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL; AB048824; BAB16711.1; -.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000636; M+channel_nlg.
DR InterPro; IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PRO1584; TASKCHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 301 AA; 32811 MW; 265DE38DFA79595E CRC64;

```

Query Match 63.6%; Score 1298.5; DB 11; Length 301;  
 Best Local Similarity 85.0%; Pred. No. 4.2e-113;  
 Matches 256; Conservative 6; Mismatches 22; Indels 17; Gaps 2;

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OY 111 MFYALGIPLTVMFOSLGERINTLVRYLLHRAKRGIGRRADVANNVLTGFESCIST 170
DB 1 MFYALGIPLTVMFOSLGERINTLVRYLLHRAKRGIGRRADVANNVLTGFESCIST 60
OY 171 LCIIGAAAFSYERMTFOAYYYCFTLTITIGFDYVALQKDALQTOPQYVAFSYIIT 230
DB 61 LCIIGAAAFSYERMTFOAYYYCFTLTITIGFDYVALQKDALQTOPQYVAFSYIIT 120
OY 231 GLTVIGAFILNVLVLRMTNNAEDEKDAEHRALLTRNGOAGGGG-----GGSAAHTT 282
DB 121 GLTVIGAFILNVLVLRMTNNAEDEKDAEHRALLTRNGOAGGGG-----GGSAAHTT 180
OY 283 DTRASSTAA-----GGGFRNRYAEVLHFOQSMCCLMYKSRKLOYSIPMITPRDL 333
DB 181 DPTVCAAAAGMGVGVGSGSFRNRYAEVLHFOQSMCCLMYKSRKLOYSIPMITPRDL 240
OY 334 STSDTCVEHSHSGGGGRYSDTPSRRLCSGAPRSATSVSTGLSLSTFRGLMKRRSS 393
DB 241 STSDTCVEHSHSGGGGRYSDTPSRRLCSGAPRSATSVSTGLSLSTFRGLMKRRSS 300
OY 394 V 394
DB 301 V 301

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## RESULT 4

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OY 0923V6 PRELIMINARY; PRT; 396 AA.
AC 0923V6:
DT 01-DEC-2001 (Tremblrel. 19, Created)

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DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Potassium channel TASK-3.  
 GN KCNK9.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSTAR;  
 RA Czarjak G., Kovacs E., Veres I., Enyedi P.;  
 RT "TASK-3 dominates the background potassium conductance in rat adrenal  
 glomerulosa cells."  
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF31084; AAK69764.1;  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR Pfam: PF00520; Ion\_Trans; 1.  
 DR PRINTS: PRO1584; TASK3CHANNEL.  
 DR PRINTS: PRO1585; TASK3CHANNEL.  
 SO SEQUENCE 396 AA; 44357 MW; 734EB0EAE1ED1828 CRC64;

Query Match 48.9%; Score 999; DB 11; Length 396;  
 Best Local Similarity 70.8%; Pred. No. 5.9e-85;  
 Matches 189; Conservative 32; Mismatches 46; Indels 0; Gaps 0;

OY 1 MKRONVRLALIVCTFTYLLGAAVFDALSEPELIERORLELROQELRARNISOGYE 60  
 DB 1 MKRONVRLSLIACFTYLLGAAVFDALSEPELIERORLELROQELRARNISOGYE 60  
 OY 61 ELERVVLRKPKKAGVOMRFGSFYATVTTTIGYGAAPSTDGKVCFCFALLGIPL 120  
 DB 61 QLELVIIQSEPHRAGVOMRFGSFYATVTTTIGYGAAPSTDGKVCFCFALLGIPL 120  
 OY 121 TLVFGSGERINTLVRYLHRKKGICMRADVSMMNVLIIGFSCISTLCIGAAFSH 180  
 DB 121 TLVFGSGERINTLVRYLHRKKGICMRADVSMMNVLIIGFSCISTLCIGAAFSH 180  
 OY 181 YEHWTFPQAYYYCFTLTITIGFGDVVALQKQALOTOPQYAFSVYILTGITVIGARLN 240  
 DB 181 CEDSFFHAYYYCFTLTITIGFGDVVALQKQALORPFPYAFSEMYILVGLTVIGARLN 240  
 OY 241 LVVLRFTMTNADEKRDARHALLTRN 267  
 DB 241 LVVLRFTMTNDEDLLEGEVAOIIAGN 267

RESULT 5

OY 09JUL04 PRELIMINARY; PRT; 395 AA.  
 AC 09JUL04;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Potassium channel TASK3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=CEREBELLUM;  
 RX MEDLINE=20200422; PubMed=10734076;  
 RA Kim Y., Bang H., Kim D.;  
 RT "TASK-3, a New Member of the Tandem Pore K+ Channel Family."  
 RL J. Biol. Chem. 275:9340-9347(2000).  
 DR EMBL: AF192366; AAF60229.1;  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR003092; TASK3CHANNEL.  
 DR Pfam: PF00520; Ion\_Trans; 1.

DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR PRINTS: PRO1584; TASK3CHANNEL.  
 DR PRINTS: PRO1585; TASK3CHANNEL.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 SO SEQUENCE 395 AA; 44365 MW; 3F76F7923A3AFC76 CRC64;

Query Match 47.0%; Score 960.5; DB 11; Length 395;  
 Best Local Similarity 69.7%; Pred. No. 2.3e-81;  
 Matches 186; Conservative 31; Mismatches 49; Indels 1; Gaps 1;

OY 1 MKRONVRLALIVCTFTYLLGAAVFDALSEPELIERORLELROQELRARNISOGYE 60  
 DB 1 MKRONVRLSLIACFTYLLGAAVFDALSEPELIERORLELROQELRARNISOGYE 60  
 OY 61 ELERVVLRKPKKAGVOMRFGSFYATVTTTIGYGAAPSTDGKVCFCFALLGIPL 120  
 DB 61 QLELVIIQSEPHRAGVOMRFGSFYATVTTTIGYGAAPSTDGKVCFCFALLGIPL 120  
 OY 121 TLVFGSGERINTLVRYLHRKKGICMRADVSMMNVLIIGFSCISTLCIGAAFSH 180  
 DB 121 TLVFGSGERINTLVRYLHRKKGICMRADVSMMNVLIIGFSCISTLCIGAAFSH 179  
 OY 181 YEHWTFPQAYYYCFTLTITIGFGDVVALQKQALOTOPQYAFSVYILTGITVIGARLN 240  
 DB 180 CEDSFFHAYYYCFTLTITIGFGDVVALQKQALORPFPYAFSEMYILVGLTVIGARLN 239  
 OY 241 LVVLRFTMTNADEKRDARHALLTRN 267  
 DB 240 LVVLRFTMTNDEDLLEGEVAOIIAGN 266

RESULT 6

OY 09ES08 PRELIMINARY; PRT; 237 AA.  
 AC 09ES08;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Two pore potassium channel KT3.2 (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=21324619; PubMed=11431495;  
 RA Vega-Saenz De Miera E., Lau D.H.P., Zhadina M., Pountney D.,  
 RA Coetzee W.A., Rudy B.;  
 RT "Kt3.2 and kt3.3, two novel human two-pore k(+) channels closely  
 related to TASK-1."  
 RL J. Neurophysiol. 86:130-142(2001).  
 DR EMBL: AF257082; AAG33128.1;  
 DR InterPro: IPR003280; K+channel\_2pore.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR003092; TASK3CHANNEL.  
 DR Pfam: PF00520; Ion\_Trans; 1.  
 DR PRINTS: PRO1333; 2PORECHANNEL.  
 DR PRINTS: PRO1584; TASK3CHANNEL.  
 DR PRINTS: PRO1585; TASK3CHANNEL.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 KW Ionic channel.  
 FT NON\_TER 237 237  
 SO SEQUENCE 237 AA; 26674 MW; A44D2D32BE08A7DB CRC64;

Query Match 45.2%; Score 924; DB 11; Length 237;  
 Best Local Similarity 73.4%; Pred. No. 3.1e-78;  
 Matches 174; Conservative 26; Mismatches 37; Indels 0; Gaps 0;

OY 1 MKRONVRLALIVCTFTYLLGAAVFDALSEPELIERORLELROQELRARNISOGYE 60  
 DB 1 MKRONVRLSLIACFTYLLGAAVFDALSEPELIERORLELROQELRARNISOGYE 60





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RP SEQUENCE FROM N.A.
RA Lovell J.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Preisig-Mueller R., Rajan S., Derst C.;
RT "Cloning and sequencing of a novel tandem pore domain potassium
   channel (TASK-4).";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A119522; CAC14068.1; -
DR EMBL: AF294352; AK97093.1; -
DR EMBL: AF294351; AK97092.1; -
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003092; TASK_channel.
DR Pfam: PF00520; Ion_trans.1.
DR PRINTS: PR01333; ZPORECHANNEL.
DR PRINTS: PR01095; TASKCHANNEL.
KM Ionic channel.
SQ SEQUENCE 330 AA; 36222 MW; 24F428721A1C7790 CRC64;

Query Match 41.0%; Score 838; DB 4; Length 330;
Best Local Similarity 64.3%; Pred. No. 5.2e-70;
Matches 166; Conservative 32; Mismatches 60; Indels 0; Gaps 0;

QY 1 MKRQNVTLALIVCTFTYLLVGAAVFDALSEPELIRQRLERQDELRLARYNLSCGYE 60
DB 1 MKRPSVAAAGLVCTCTCYLLVGAAVFDALSEAGSGRQLLYOKRGALRRKFGFSADYR 60
QY 61 ELERVVRLRPHKAGVOMRFGSGFYFAITVITTYIGYHAAPSTDGKVFCEFTALLGIP 120
DB 61 ELERLALQAPRHAGRQMKRPGSFYFAITVITTYIGYHAAPSTDGKVFCEFTALLGIP 120
QY 121 TLVFGSLGRINLTAVLLHRAKKGIMRADVSMANMVLIGFSCISTLCIGAAAFSH 180
DB 121 TLVTFOSLGRINLTAVLLHRAKKGIMRADVSMANMVLIGFSCISTLCIGAAAFSH 180
QY 181 YEHWTFQAYVYCCFTLTITGFGDYVALQKDALQLOPOVYAFSEVYLLGLTVIGAF 240
DB 181 FEGHTFPHAYTCFTLTITGFGDYVALQSGEALQRLPYAFSEFTLLGLTVIGAF 240
QY 241 LVVLRFTMNAEDEKRD 258
DB 241 LVVLRFLVASADMPERRA 258

RESULT 10
017185 PRELIMINARY; PRT; 329 AA.
ID 017185
AC 017185: 076795;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 37.0 kDa protein (Putative potassium channel subunit
   n2P38).
GN F34D6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; Pubmed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
   investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=20196006; Pubmed=10731132;
RA Murray J., Wohlmann P., O'Neal D.;

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RT "The sequence of C. elegans cosmid F34D6.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Wang Z.-W., Salkoff L.;
RT "Potassium channels in C. elegans.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF025454; AAC71151.2; -
DR EMBL: AF083652; AAC32863.1; -
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003092; TASK_channel.
DR Pfam: PF00520; Ion_trans.1.
DR PRINTS: PR01333; ZPORECHANNEL.
DR PRINTS: PR01095; TASKCHANNEL.
KM Hypothetical protein; Ionic channel.
SQ SEQUENCE 329 AA; 36992 MW; 338A6D9A577464CD CRC64;

Query Match 40.2%; Score 820; DB 5; Length 329;
Best Local Similarity 48.3%; Pred. No. 2.5e-68;
Matches 172; Conservative 54; Mismatches 84; Indels 46; Gaps 7;

QY 1 MKRQNVTLALIVCTFTYLLVGAAVFDALSEPELIRQRLERQDELRLARYNLSCGYE 60
DB 1 MKRQNVTLALIVCTFTYLLVGAAVFDALSEPELIRQRLERQDELRLARYNLSCGYE 60
QY 61 ELERVVRLRPHKAGVOMRFGSGFYFAITVITTYIGYHAAPSTDGKVFCEFTALLGIP 120
DB 61 ELERVVRLRPHKAGVOMRFGSGFYFAITVITTYIGYHAAPSTDGKVFCEFTALLGIP 120
QY 121 TLVFGSLGRINLTAVLLHRAKKGIMRADVSMANMVLIGFSCISTLCI--GAAAF 178
DB 121 TLVFGSLGRINLTAVLLHRAKKGIMRADVSMANMVLIGFSCISTLCI--GAAAF 178
QY 179 SHEHWTFQAYVYCCFTLTITGFGDYVALQKDALQLOPOVYAFSEVYLLGLTVIGAF 238
DB 179 SHEHWTFQAYVYCCFTLTITGFGDYVALQKDALQLOPOVYAFSEVYLLGLTVIGAF 238
QY 238 MNLVLRFTMNAEDEKRD 294
DB 238 MNLVLRFTMNAEDEKRD 294
QY 295 GFRVVAEVLHFGSCGLWYKSKREKLOYSLPMTIPRDLSTSDCVFQSSHPGCG 350
DB 295 GFRVVAEVLHFGSCGLWYKSKREKLOYSLPMTIPRDLSTSDCVFQSSHPGCG 350
QY 350 GFRVVAEVLHFGSCGLWYKSKREKLOYSLPMTIPRDLSTSDCVFQSSHPGCG 350
DB 350 GFRVVAEVLHFGSCGLWYKSKREKLOYSLPMTIPRDLSTSDCVFQSSHPGCG 350

RESULT 11
09VHEO PRELIMINARY; PRT; 340 AA.
ID 09VHEO
AC 09VHEO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG9361 protein.
GN CG9361.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.;

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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zbair N., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blaze G., Champagne M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Burris K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Moberly C., Morris J., Moshireti A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazolo M., Pittman K.S., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003682; AAF54374.1; -;  
 DR FlyBase: Fggn0037690; CG9361.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR003092; TASK\_channel.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 DR PRINTS: PRO1586; THIRCHANNEL.  
 SQ SEQUENCE 340 AA; 37840 MW; 018D756D21F8D57A CRC64;

Query Match 38.1%; Score 777; DB 5; Length 340;  
 Best local similarity 47.7%; Pred. No. 2.7e-64;  
 Matches 166; Conservative 48; Mismatches 118; Indels 16; Gaps 5;

OY 1 MKRONVRLALIVCTFTYLLVGAANFVALESEBELIERORLELROELRARNYLSGGYE 60  
 DB 2 MKRONVRLSLVCTFTYLLVGAANFVALESEBELIERORLELROELRARNYLSGGYE 61  
 OY 61 ELERVVLAKPRKAGQMPFASFPATVITTTIGYGAHPSTDGKVCYMFALGIFL 120  
 DB 62 VWEIVIEIKPKAGQMPFASFPATVITTTIGYGAHPSTDGKVCYMFALGIFL 121  
 OY 121 TLMVFOSLGERINTVRLVLLHRAKGLGMRADVSANVNL-IGFSCSTLTCIGAAAS 179  
 DB 122 GLVMFOSLGERINTVRLVLLHRAKGLGMRADVSANVNL-IGFSCSTLTCIGAAAS 180  
 OY 180 HVEHMTFOAYVYVCTFTTITGFDVVALQKDOALOTOPQVYAFSEVYLLTGLTVIGAF 239  
 DB 181 RREGMSYFDSFYCYFTLTITGFDVVALQKDOALOTOPQVYAFSEVYLLTGLTVIGAF 240  
 OY 240 NLVYLFMTMADEKRAEHRALLTRNGAGGGGGGSAHTTTRASTAAAGGGGFRNV 299  
 DB 241 NLVYLFMTMADEKRAEHRALLTRNGAGGGGGGSAHTTTRASTAAAGGGGFRNV 299  
 OY 300 Y-AYVLHFGMSCLMYKSRKLT---QYSIPMIIPRDLSTDTCTEVS 343

DB 291 YTTENDETASLSCCTCMGCTRCINHEQFVDPDFOPPTDIESTICLKRA 338  
 RESULT 12  
 ID Q9VFS9 PRELIMINARY; PRT; 398 AA.  
 AC Q9VFS9;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE CG9637 protein.  
 GN CG9637.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blaze G., Champagne M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Burris K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Moberly C., Morris J., Moshireti A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazolo M., Pittman K.S., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003701; AAF54970.1; -;  
 DR FlyBase: Fggn0038165; CG9637.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR003092; TASK\_channel.  
 DR Pfam: PF00520; Ion\_trans\_1.  
 DR PRINTS: PRO1095; TASKCHANNEL.  
 SQ SEQUENCE 398 AA; 44269 MW; D5DC011E9BDA6D7E CRC64;  
 Query Match 36.3%; Score 742; DB 5; Length 398;  
 Best local similarity 42.8%; Pred. No. 6.2e-61;  
 Matches 161; Conservative 65; Mismatches 76; Indels 74; Gaps 9;

```

Db 1 MKGNVATRIISLVTCTFYLLVGAVALFALBSETEKRRMEALQDAEDMIIRKYNISQDEFK 60
OY 61 ELEENVLRKPKHKGVMQRFAGSFYFAITVTITGCGAAPTSTGCKVCFYALLGIP 120
Db 61 VMETVYKSESHKAGQOMKFTGAFYATVTITGCGHSTPSTGKFTMCYAVIGIPL 120
OY 121 TLVVFOSLGERINTLVRLHRAKKGLGMRADVSMANMVLIGFSCSTICI--GAAAF 178
Db 121 GLVVFOSIGER-----AVRSSLRCKRTVASVDLICY--VTLLSSLTIGGAFAF 168
OY 179 SHVEHMTFFQAYVYCFITLTITGFGDYVALQKDALOTOPQYVAFSEFYILTGLVIGAF 238
Db 169 SKFEGWSEYFDSYVYCFITLTITGFGDMVALORDNALNRKPEYVAFILIFGLALVAA 228
OY 239 LNLVLRFTMTNADKRDARHRL-----LTRNGAGGGGGGSAHTTDTA 285
Db 229 LNLVLRFTMTNDEDERD--EAQAMQALQYAVKLEGDVITSNGSILSGEGHDCQSILNG 287
OY 286 SSTAAAGGGCFRNYAEVLHFGSMCSC-----LWYKSREK-- 320
Db 288 NTS-----SMCSCHICICLGNRHKSSNLKKNDAENQYRLROSPT 328
OY 321 -LOYSIPIIP-RDLS 334
Db 329 HIRHLPEVPMODLN 344

```

## RESULT 13

```

OY 09JL57 PRELIMINARY; PRT; 270 AA.
AC 09JL57;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Potassium channel TASK3 (Fragment).
GN KCNK9.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
NC NCBL_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20287530; PubMed=10747866;
RA Rajan S., Mischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
RA Karschin A., Dersic C.;
RT "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An
RT extracellular histidine as pH sensor.";
RL J. Biol. Chem. 275:16650-16657 (2000).
DR EMBL: AF212828; AAF63707.1; -
DR InterPro: IPR001622; K-channel_pore.
DR InterPro: IPR000636; K-channel_nlg.
DR InterPro: IPR003092; TASK_channel.
DR Pfam: PF00520; Ion_Trans; 1.
DR PRINTS: PRO1584; TASK1CHANNEL.
DR PRINTS: PRO1585; TASK3CHANNEL.
DR PRINTS: PRO1095; TASKCHANNEL.
FT NON_TER 1
SQ SEQUENCE 270 AA; 29858 MW; 092ABFEC7BC1E56 CRC64;

Query Match 35.9%; Score 732.5; DB 11; Length 270;
Best Local Similarity 54.2%; Pred. No. 2.9e-60;
Matches 163; Conservative 26; Mismatches 79; Indels 33; Gaps 6;

```

```

Db 121 RKPFFVAFSEFYILVGLVIGAFNLVYLRLLTNNSDEREGEGCALP-----GNPS 174
OY 276 GCSAHTDTASTAA--AGGGCFRNYAEVLHFGSMCSCLYKSKREKIQIYIPMIPDL 333
Db 175 SVVTHISEARQVORRYREGG-----DLQSVCSACACYSQP--QNGCATLAPPL 223
OY 334 STSDTCVQSHSSPFGGGGRYSDTPSRCLCGARSATSSVSTGLHSLSTRGLMKRRSS 393
Db 224 HSICRIEET-----SPS--TLKNSLPSPSSVSPGLHSGDNHRLMRKS 269
OY 394 V 394
Db 270 V 270

```

## RESULT 14

```

OY 0920G1 PRELIMINARY; PRT; 237 AA.
AC 0920G1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Tandem acid-sensitive potassium channel TASK5 (Fragment).
GN KCNK15.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NC NCBL_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WISTAR;
RA Preisig-Mueller R., Rajan S., Dersic C.;
RT "Cloning and sequencing of a novel tandem pore domain potassium
RT channel (TASK-4).";
RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF294353; AAK97094.1; -
DR InterPro: IPR001622; K-channel_pore.
DR InterPro: IPR000636; K-channel_nlg.
DR Pfam: PF00520; Ion_Trans; 1.
DR PRINTS: PRO1584; TASK1CHANNEL.
KM Ionic channel.
FT NON_TER 1
FT NON_TER 237
SQ SEQUENCE 237 AA; 26158 MW; 7B39915663C98DEF CRC64;

```

```

Query Match 33.8%; Score 690.5; DB 11; Length 237;
Best Local Similarity 73.3%; Pred. No. 2.1e-56;
Matches 137; Conservative 17; Mismatches 33; Indels 1; Gaps 1;

```

```

OY 82 GSFYFAITVTITGCGAAPTSTGCKVCFYALLGIPLTVMFOSLGERINTLVRYLLH 141
Db 1 GSFYFAITVTITGCGAAPTSTGCKVCFYALLGIPLTVMFOSLGERINALVRCILL 60
OY 142 RAKKGLGMRADVSMANMVLIGFSCSTICI--GAAAFSHVEHMTFFQAYVYCFITLTITG 201
Db 61 AAKKCLGRRRHVSANMNVAGLLCAATLALGAAAFHFGKTFPFAHYVYCFITLTITG 120
OY 202 FGDYVALQKDALOTOPQYVAFSEFYILTGLVIGAFNLVYLRFTMTNADKRDARH 261
Db 121 FGDYVALQKDALQKPPYVAFSEFYILTGLVIGAFNLVYLRFLA--SAEAPERALAR 179
OY 262 ALLTRNG 268
Db 180 ASVFRRG 186

```

## RESULT 15

```

OY 076790 PRELIMINARY; PRT; 364 AA.
AC 076790;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

```

DE 01.MAR-2002 (TREMBLE). 20, last annotation update)  
DT Putative potassium channel subunit N2P20.  
GN TKK-4.  
OS *Caenorhabditis elegans*.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae.  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang Z.-W., Salkoff L.;  
RT "Potassium channels in *C. elegans*."  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hembrly C.;  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "genome sequence of the nematode *C. elegans*: A platform for  
RT investigating biology".  
RL Science 282:2012-2018(1998).  
DR EMBL; AF083646; AAC32857.1; -.  
DR EMBL; Z70266; CAB61045.1; -.  
DR InterPro: IPR003280; K+channel\_2pore.  
DR InterPro: IPR001622; K+channel\_pore.  
DR InterPro: IPR000636; M+channel\_nlg.  
DR Pfam: PF00520; Ion\_trans\_1.  
DR PRINTS: PR01333; 2PORECHANBL.  
KW Ionic channel.  
SO SEQUENCE 364 AA; 41374 MW; 4247A6050CC4313 CRC64;

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 15:14:17 ; Search time 18 Seconds  
(without alignments)  
2104.276 Million cell updates/sec

Title: US-09-939-484-4  
Perfect score: 2042  
Sequence: 1 MKRONVRLTLIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR\_73:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	41.4	330	2	JC7703 TASK-5 protein - h
2	820	40.2	329	2	T43509 probable potassium
3	806.5	39.5	336	2	T32347 outward rectifier
4	599	29.3	334	2	T19860 hypothetical prote
5	599	29.3	364	2	T43361 probable potassium
6	320.5	15.7	336	2	S65566 inward rectifier p
7	307.5	15.1	513	2	T28933 hypothetical prote
8	293	14.3	393	2	T25392 hypothetical prote
9	276.5	13.5	1910	2	H88124 protein T12C9.3 [1
10	275	13.5	524	2	T23907 hypothetical prote
11	268	13.1	1539	2	T30037 hypothetical prote
12	262	12.8	443	2	T21598 hypothetical prote
13	261.5	12.8	1001	2	T13807 potassium channel
14	258.5	12.7	335	2	S44635 f22b7.7 protein -
15	258.5	12.7	427	2	T27681 hypothetical prote
16	258	12.6	383	2	T23182 hypothetical prote
17	256.5	12.6	452	2	T21118 hypothetical prote
18	251	12.3	544	2	T43363 potassium channel
19	251	12.3	576	2	T43363 potassium channel
20	250	12.2	569	2	T43531 probable potassium
21	248	12.1	444	2	T26229 hypothetical prote
22	247.5	12.1	392	2	T45032 hypothetical prote
23	245	12.0	769	2	T27550 hypothetical prote
24	244	11.9	381	2	T43393 potassium channel
25	243	11.9	528	2	T21834 hypothetical prote
26	239.5	11.7	522	2	T24265 hypothetical prote
27	235.5	11.5	475	2	T27725 hypothetical prote
28	234.5	11.5	485	2	T24201 hypothetical prote
29	231.5	11.3	484	2	T43529 probable potassium

30	231.5	11.3	519	2	T16629 hypothetical prote
31	229	11.2	325	2	T15584 hypothetical prote
32	229	11.2	461	2	T43394 potassium channel
33	222.5	10.9	600	2	T24626 hypothetical prote
34	216	10.6	350	2	T15178 hypothetical prote
35	215.5	10.6	643	2	T26616 hypothetical prote
36	211	10.3	539	2	T23700 hypothetical prote
37	210.5	10.3	504	2	T23269 hypothetical prote
38	210	10.3	1136	2	T26953 hypothetical prote
39	205.5	10.1	586	2	T21683 hypothetical prote
40	201.5	9.9	551	2	T16426 hypothetical prote
41	201.5	9.9	555	2	T43357 potassium channel
42	200.5	9.8	700	2	T27364 hypothetical prote
43	199.5	9.8	660	2	T21551 hypothetical prote
44	193.5	9.5	523	2	T23373 hypothetical prote
45	190.5	9.3	383	2	T23746 hypothetical prote

ALIGNMENTS

```
RESULT 1
JC7703
TASK-5 protein - human
C:Species: Homo sapiens (man)
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: JC7703
R:Kim, D.; Gnatenco, C.
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A>Title: TASK-5, a new member of the tandem-pore K+ channel family.
A:Reference number: JC7703; MUID:21303050; PMID:11409881
A:Accession: JC7703
A:Molecule type: DNA
A:Residues: 1-330 <KIN>
A:Cross-references: GB:AL118522
A:Comment: This protein, a new member of the tandem-pore K+ channel family with four
hormone secretion, but does not produce a functional plasma membrane K+ current by it
C:Genetics:
A:Gene: task-5
A:Map position: 20q12
C:Keywords: transmembrane protein
F:7-30/Domain: transmembrane segment #status predicted <TMS1>
F:107-158/Domain: transmembrane segment #status predicted <TMS2>
F:126-155/Region: hydrophobic cytoplasmic linker #status predicted
F:156-180/Domain: transmembrane segment #status predicted <TMS3>
F:220-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match
Best Local Similarity 64.7%; Pred. No. 1.7e-69; Length 330;
Matches 167; Conservative 32; Mismatches 99; Indels 0; Gaps 0;

OY 1 MKRONVRLTLIVCTFTYLLVGAAYDALSEPELIERORLELROELRARNLSQGYE 60
DB 1 MRRPSVRAAGLVLCYLVGAAYFDALSEAESGRORLVLQKGRARRRFGSAEDYR 60
OY 61 ELERVVLTKRKHKAGVQKRFAGSFYFATVTTTGGYGAASSTOGKRFYVNLGIP 120
DB 61 ELERVVLTKRKHKAGVQKRFAGSFYFATVTTTGGYGAASSTOGKRFYVNLGIP 120
OY 121 TLVVFOSGERINTLVRYLHRAKAGLGMRRADVSMMANNVIGFSPCISTCIGAAFSH 180
DB 121 TLVVFOSGERINTLVRYLHRAKAGLGMRRADVSMMANNVIGFSPCISTCIGAAFSH 180
OY 181 YEHMTFFQAYVYCFITLTTFGSDVALQDQALQTOPOYVAFSFTVILGLVYIGAF 240
DB 181 YEHMTFFQAYVYCFITLTTFGSDVALQDQALQTOPOYVAFSFTVILGLVYIGAF 240
OY 241 LVVLRFTMNADEKRD 258
DB 241 LVVLRFTMNADEKRD 258
OY 258 LVVLRFTMNADEKRD 258
DB 258 LVVLRFTMNADEKRD 258
```





C:Species: *Caenorhabditis elegans*  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
C:Accession: T43361  
R:Mang, Z.W.; Salkoff, L.  
submitted to the EMBL Data Library, August 1998  
A:Description: Potassium channels in *C. elegans*.  
A:Reference number: 222450  
A:Accession: T43361  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-364 <MAN>  
A:Cross-References: EMBL:AF083646, PIDN:AAC32957.1

Query Match	599	DB 2	Length	364					
Best Local Similarity	46.18	Pred. No.	7.3e-47						
Matches	119	Conservative	46	Mismatches	81	Indels	12	Gaps	3

```

QY  QANRTALTYCPTTYLLVLAFAADLIESPELIEQRLELNOQELRARNYNSOGYBELE 63
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  7 KSRALLLLISTPTTYLLFEGAMVFDKLESKODVWVDELERITDRKHKRYNSENDLHFE 66
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  64 RVLRLRKPKAQVMRFAGSEFYFAITVTITTYIGYHAAESTDGRKVCMAFYALLGIPLLV 123
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  67 AIAIKSIPDOAGYOMOFACAFYFAATVTITVTVYGSHAPSTNAGKLFCMIFALFVPMGLI 126
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  124 MPAISGERINTLVRYLLHRAKKGGLGMR----RADVSAMNML----IGFECISITLIGA 175
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  127 MPOSIGERNTFTANSLHFRDLSLHQOGTCLQETVPHLLMVSILITGEMVIVS---GT 182
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  176 AAEHSYEHMTFQOAYFCTITLTITGFGDYVALQKDALQOPQVYAFSEFYVITGLTVI 235
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  183 YMFHTIEKMSIFPAYFYCMITESTJTGFGDVLPLQOVNALQOQPLVYFATIMFILIGLAVF 242
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  236 GAFNLVLVLRFTMTNAD 253
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  243 SACCINLLVGLGFMASNADE 260
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 6
S65566
Inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S65566
R:Release: F.; Gullenmare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin,
EMBO J. 15, 1004-1011, 1996
A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel s
A:Reference number: S65566; MUID:96183184; PMID:8605869
A:Accession: S65566
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: EMBL:U33632; NID:G1086490; PIDN:AB01688.1; PID:G1086491

```

Query Match	15.7%	Score 320.5;	DB 2;	Length 336;
Best Local Similarity	32.4%	Pred. No. 1.9e-21;		
Matches 90;	Conservative 47;	Mismatches 102;	Indels 39;	Gaps 9;

QY 11 IYCTFFYLLYGAAVFADLSEPELIERQRL-ELRQOELRAKYNISOGYEELERVLRL 69  
 Db 26 LVGLGALLLVGAAVFSSVLEPEDLRLKRLRLEEHCECISEOOLEQFLGRVLEA 85  
 QY 70 KPRKAGV-----QRRFAGSFYPAIVITTTGGYGHASPDSGKVCMPFALLGIPLT 121  
 Db 86 SNYGVSVLNMSGNNMDFLTALFPASTYVLTSTTGGHYVPLSDGSKACIIYSYVIGIPT 145  
 QY 122 LVMFQSLGERINTLVRYLLHRAKKGL-----GMRADYSMANVLLGFESICSTLCIG 174  
 Db 146 LLFLTAAYVQRT-----VHYTRRPELVFHHIRMGSKOVAIVAHVLLGFVTVSCFFIP 199  
 QY 175 AAASHEV-HHTFQAYVYCFITLTITIGEGDVA-----LQDQALQTPQRYAFSEFVYL 229  
 Db 200 AAASFVLEDDNNFESFEFCSITSTIGLGDVPEEGYNQKFRRL-----XKIGITWYLL 254

QY 230 TG----LTVTGAFNLNVL---RPTMNAAEDEKRDAEH 260  
| | : | | | : | |  
Db 255 IGLIAMLVNIETFCELHELAKKFKRMFYVKKDQDEQVH 292

RESULT 7  
T28933  
hypothetical protein C52B9.6 - *Caenorhabditis elegans*

A; Introns: 12/3; 54/3; 90/3; 158/1; 173/1; 227/3; 299/3; 346/2; 378/2; 405/1; 452/3

[illegible]

RESULT 8  
T25392  
hypochemical protein T28A8.1 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T25392  
R:Liroy, C.  
submitted to the EMBL Data Library, March 1997  
;Reference number: Z20027

A:Accession: T23592  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-393 <MIL>  
A:Cross-references: EMBL:292813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T28A8.1  
A:Experimental source: clone T28A8  
C:Genetics:  
A:Gene: CESP:T28A8.1  
A:Map position: 3  
A:Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2

Query Match 14.3%; Score 293; DB 2; Length 393;  
Best Local Similarity 26.6%; Pred. No. 7.7e-19;  
Matches 78; Conservative 57; Mismatches 96; Indels 62; Gaps 9;

OY 9 LALIVCTFTYLVGAAPFALSEPEL-----IERQRLERL----- 45  
DB 15 VSLIVSVYVYGALFYLQLEQNEVEVARNIERPNHKKOMIEHLMEMRESGIGHV 74  
OY 46 -DELARY--NLSQGYEELERVLRKPKAG---VQMRFGSFYATVITIGYG 97  
DB 75 VEDLAKYVDNVRIRLFEAFDHCIGAKHLRPGCEDENWMTMALFTTILITIGYG 134  
OY 98 HAAPSTDGKRVCFMAYALLGIPITLVFQSLGERI--NTLVRYLHR----- 142  
DB 135 NLTPVYGRKLLCILYALFGVPLILTVADIGKFLSENIVQLTWYRKLRKCKSKOYSY 194  
OY 143 -AKKGGMRADY--MANMVLIGFSCI---STLCGAANFSYEHMTFQAYYCP 194  
DB 195 ISKDKRKEGDLNDHLENYISIPFLVAILSTTTCGAVVLSMEGDFSGFYFSF 254  
OY 195 ITLTIGFDYVALQKDALQTOPQYVAFSEFVYILGLVYGAFLNVLVRFM 247  
DB 255 IFMTVTGFGDIYELKR-----EYIIDLCTIITIGLSTTMCIDLVIQYI 299

RESULT 9  
H88124  
protein T12C9.3 (imported) - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: H88124  
R:anonymous, The C. elegans Sequencing Consortium.  
A:title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; MID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: H88124  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1910 <STO>  
A:Cross-references: GB:chr\_II; PIDN:AC71141.1; PID:q1086770; GSPDB:GN00020; CESP:T12C9.3  
C:Genetics:  
A:Gene: T12C9.3  
A:Map position: 2

Query Match 13.5%; Score 276.5; DB 2; Length 1910;  
Best Local Similarity 23.3%; Pred. No. 1.7e-16;  
Matches 80; Conservative 49; Mismatches 107; Indels 107; Gaps 8;

OY 4 QNVRTLA-----LIVCTFTYLVGAAPFALSEPELIERQRLERLROOELARVN 53  
DB 189 QNIRKAKLALPHIVVVCVCIATIGANIFYTLESPEKDRLKETGRKTIEMRSNLTK 248  
OY 54 LS-----OGGYEELERV--VL 67  
DB 249 INNEKEVWKEDIEKELMLYSEKLYAKFQYVRSADVRTIGEGSSSYEADETGDSR 308  
OY 68 RLKPKHAG-----VQMRFGSFYATVITIGYHAAPSTDGKRVCFMAYALLGI 118  
DB 309 RRRHRHGNKRGDRGSEKMMYTSALFPAATMATIGNIVPVPLGRACVLFALFGA 368

OY 119 PLTLVNFQSLGERINTLVRYLHRKAKG-----LGMRRADVS 155  
DB 369 PIALITIGDKRLSCTITMLYKMKRGSRLDSAMKRFGLDSTSDLESASKNODS 428  
OY 156 MANM-----VLIGFSCISTLCGAANFSYEHMTFQAYYCEITLTIGFGD 204  
DB 429 ILDMDEIDKSEVPLWMTTILLYIAFGILFSLIEMSYADAFYFSISLTIGFGD 488  
OY 205 YVALQKDALQTOPQYVAFSEFVYILGLVYGAFLNVLVRFM 247  
DB 489 IYPENHD-----YIALMLYLVGSLSTTMCIDLVIQYI 523

RESULT 10  
T23907  
hypoetical protein R04F11.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T23907  
R:Harris, B.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19816  
A:Accession: T23907  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-524 <MIL>  
A:Cross-references: EMBL:27475; PIDN:CAA8957.1; GSPDB:GN00023; CESP:R04F11.4  
A:Experimental source: clone R04F11  
C:Genetics:  
A:Gene: CESP:R04F11.4  
A:Map position: 5  
A:Introns: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1; 489/2

Query Match 13.5%; Score 275; DB 2; Length 524;  
Best Local Similarity 23.3%; Pred. No. 4.8e-17;  
Matches 88; Conservative 38; Mismatches 92; Indels 150; Gaps 9;

OY 11 LIVCTFTYLVGAAPFALSEPELIERQRLERLROOELARVN----- 52  
DB 18 LVTLSTGYTLIGALCFHHEKPEYEQQLRNETSRIGELKRVNDQLMBSNNGTAVSTNR 77  
OY 53 NLSQGYEELERVVL-----RLKPH-----KAGVQMRFGSFYATVITIGYHAAP 101  
DB 78 QFANDMDEIDRVDYFDTYRNYMTPDVYIGDPIKMSFMSIFSWTAITTIGYHIYP 137  
OY 102 STDGKRVCFMAYALLGIPITLVFQSLGERINTLV----- 136  
DB 138 RTDEGRVAILFYALLGIPILTVIADIGRLATYIIKLHGYMAVNSFVTSNCLKICIKMA 197  
OY 137 -----RY-----LLHRAK-----GLGMR----- 150  
DB 198 CCMIRLPKRHIIMPTLELLQRTQKLPNNNNPVAATAASAGGCTRRKKQQRDNVSDAG 257  
OY 151 -----RV-----RADVSMANMVLIGFSCISTLCIG 174  
DB 258 TFDNISEINDSGENENGEDEEQIQDPNSHKEKRVVLFLLIMLGY-----VAGG 311  
OY 175 AAASFYEHMTFQAYYCEITLTIGFGDYVALQKDALQTOPQYVAFSEFVYILGLV 234  
DB 312 AYIYRWEMETFEAFYFCFVYVTTIGFDIVPAND-----WLPATLAIYVGLII 363  
OY 235 IGAFLNVL 242  
DB 364 TTMCIDLV 371

RESULT 11  
T30037  
hypoetical protein F20A1.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T30037





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:15:48 ; Search time 26 Seconds  
(without alignments)  
1661.571 Million cell updates/sec

Title: US-09-939-484-4  
Perfect score: 2042  
Sequence: 1 MKRONVRLTALIVCTFTYLL.....STGLHSLSTRGLMKRRSSV 394

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
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12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	10 US-09-939-484-4	Sequence 4, Appl1
2	2042	100.0	394	10 US-09-939-483-4	Sequence 4, Appl1
3	2042	100.0	394	10 US-09-798-584-15	Sequence 15, Appl1
4	1819	89.1	405	10 US-09-939-484-5	Sequence 5, Appl1
5	1819	89.1	405	10 US-09-939-483-5	Sequence 5, Appl1
6	1278	62.6	258	10 US-09-746-491-61	Sequence 61, Appl1
7	1116	54.7	374	10 US-09-798-584-1	Sequence 1, Appl1
8	1069.5	52.4	365	10 US-09-746-491-60	Sequence 60, Appl1
9	846	41.4	330	10 US-09-746-491-59	Sequence 59, Appl1
10	838	41.0	330	10 US-09-746-491-58	Sequence 58, Appl1
11	838	41.0	330	10 US-09-746-491-57	Sequence 57, Appl1
12	774	37.9	279	10 US-09-746-491-22	Sequence 22, Appl1
13	370	18.1	370	10 US-09-864-761-34389	Sequence 34389, A
14	370	18.1	370	10 US-09-939-483-8	Sequence 8, Appl1
15	369	18.1	411	10 US-09-939-483-8	Sequence 8, Appl1
16	363	17.8	411	9 US-10-828-746-6	Sequence 6, Appl1
17	363	17.8	411	9 US-10-121-746-63	Sequence 83, Appl1
18	361	17.7	294	9 US-09-828-746-2	Sequence 2, Appl1
19	349.5	17.1	526	10 US-09-729-920-4	Sequence 4, Appl1

	20	349.5	17.1	538	10	US-09-729-920-5	Sequence 5, Appl1
	21	349.5 <th>17.1</th> <td>543<th>10</th><td>US-09-729-920-2</td><td>Sequence 2, Appl1</td></td>	17.1	543 <th>10</th> <td>US-09-729-920-2</td> <td>Sequence 2, Appl1</td>	10	US-09-729-920-2	Sequence 2, Appl1
	22	329.5 <th>16.1</th> <td>392<th>10</th><td>US-09-747-835A-55</td><td>Sequence 55, Appl1</td></td>	16.1	392 <th>10</th> <td>US-09-747-835A-55</td> <td>Sequence 55, Appl1</td>	10	US-09-747-835A-55	Sequence 55, Appl1
	23	329.5 <th>16.1</th> <td>393<th>9</th><td>US-10-243-035-2</td><td>Sequence 2, Appl1</td></td>	16.1	393 <th>9</th> <td>US-10-243-035-2</td> <td>Sequence 2, Appl1</td>	9	US-10-243-035-2	Sequence 2, Appl1
	24	329.5 <th>16.1</th> <td>419<th>10</th><td>US-09-828-035-2</td><td>Sequence 2, Appl1</td></td>	16.1	419 <th>10</th> <td>US-09-828-035-2</td> <td>Sequence 2, Appl1</td>	10	US-09-828-035-2	Sequence 2, Appl1
	25	329.5 <th>16.1</th> <td>419<th>10</th><td>US-09-747-835A-29</td><td>Sequence 29, Appl1</td></td>	16.1	419 <th>10</th> <td>US-09-747-835A-29</td> <td>Sequence 29, Appl1</td>	10	US-09-747-835A-29	Sequence 29, Appl1
	26	320.5 <th>15.7</th> <td>336<th>9</th><td>US-10-205-823-190</td><td>Sequence 190, App</td></td>	15.7	336 <th>9</th> <td>US-10-205-823-190</td> <td>Sequence 190, App</td>	9	US-10-205-823-190	Sequence 190, App
	27	320.5 <th>15.7</th> <td>336<th>10</th><td>US-09-939-484-2</td><td>Sequence 2, Appl1</td></td>	15.7	336 <th>10</th> <td>US-09-939-484-2</td> <td>Sequence 2, Appl1</td>	10	US-09-939-484-2	Sequence 2, Appl1
	28	320.5 <th>15.7</th> <td>336<th>10</th><td>US-09-939-483-2</td><td>Sequence 2, Appl1</td></td>	15.7	336 <th>10</th> <td>US-09-939-483-2</td> <td>Sequence 2, Appl1</td>	10	US-09-939-483-2	Sequence 2, Appl1
	29	319 <th>15.6</th> <td>499<th>10</th><td>US-09-735-169A-2</td><td>Sequence 2, Appl1</td></td>	15.6	499 <th>10</th> <td>US-09-735-169A-2</td> <td>Sequence 2, Appl1</td>	10	US-09-735-169A-2	Sequence 2, Appl1
	30	319 <th>15.6</th> <td>499<th>10</th><td>US-09-735-171A-2</td><td>Sequence 2, Appl1</td></td>	15.6	499 <th>10</th> <td>US-09-735-171A-2</td> <td>Sequence 2, Appl1</td>	10	US-09-735-171A-2	Sequence 2, Appl1
	31	295.5 <th>14.5</th> <td>313<th>9</th><td>US-10-121-746-81</td><td>Sequence 81, Appl1</td></td>	14.5	313 <th>9</th> <td>US-10-121-746-81</td> <td>Sequence 81, Appl1</td>	9	US-10-121-746-81	Sequence 81, Appl1
	32	295.5 <th>14.5</th> <td>313<th>10</th><td>US-09-735-169A-8</td><td>Sequence 8, Appl1</td></td>	14.5	313 <th>10</th> <td>US-09-735-169A-8</td> <td>Sequence 8, Appl1</td>	10	US-09-735-169A-8	Sequence 8, Appl1
	33	295.5 <th>14.5</th> <td>313<th>10</th><td>US-09-735-171A-8</td><td>Sequence 8, Appl1</td></td>	14.5	313 <th>10</th> <td>US-09-735-171A-8</td> <td>Sequence 8, Appl1</td>	10	US-09-735-171A-8	Sequence 8, Appl1
	34	294.5 <th>14.4</th> <td>332<th>10</th><td>US-09-735-169A-5</td><td>Sequence 5, Appl1</td></td>	14.4	332 <th>10</th> <td>US-09-735-169A-5</td> <td>Sequence 5, Appl1</td>	10	US-09-735-169A-5	Sequence 5, Appl1
	35	294.5 <th>14.4</th> <td>332<th>10</th><td>US-09-735-171A-5</td><td>Sequence 5, Appl1</td></td>	14.4	332 <th>10</th> <td>US-09-735-171A-5</td> <td>Sequence 5, Appl1</td>	10	US-09-735-171A-5	Sequence 5, Appl1
	36	190.5 <th>9.3</th> <td>383<th>10</th><td>US-09-939-484-7</td><td>Sequence 7, Appl1</td></td>	9.3	383 <th>10</th> <td>US-09-939-484-7</td> <td>Sequence 7, Appl1</td>	10	US-09-939-484-7	Sequence 7, Appl1
	37	190.5 <th>9.3</th> <td>383<th>10</th><td>US-09-939-483-7</td><td>Sequence 7, Appl1</td></td>	9.3	383 <th>10</th> <td>US-09-939-483-7</td> <td>Sequence 7, Appl1</td>	10	US-09-939-483-7	Sequence 7, Appl1
	38	179 <th>8.8</th> <td>39<th>10</th><td>US-09-746-491-63</td><td>Sequence 63, Appl1</td></td>	8.8	39 <th>10</th> <td>US-09-746-491-63</td> <td>Sequence 63, Appl1</td>	10	US-09-746-491-63	Sequence 63, Appl1
	39	176.5 <th>8.6</th> <td>107<th>10</th><td>US-09-828-746-4</td><td>Sequence 4, Appl1</td></td>	8.6	107 <th>10</th> <td>US-09-828-746-4</td> <td>Sequence 4, Appl1</td>	10	US-09-828-746-4	Sequence 4, Appl1
	40	156 <th>7.6</th> <td>347<th>10</th><td>US-09-939-483-6</td><td>Sequence 6, Appl1</td></td>	7.6	347 <th>10</th> <td>US-09-939-483-6</td> <td>Sequence 6, Appl1</td>	10	US-09-939-483-6	Sequence 6, Appl1
	41	156 <th>7.6</th> <td>347<th>10</th><td>US-09-939-483-6</td><td>Sequence 6, Appl1</td></td>	7.6	347 <th>10</th> <td>US-09-939-483-6</td> <td>Sequence 6, Appl1</td>	10	US-09-939-483-6	Sequence 6, Appl1
	42	131.5 <th>6.4</th> <td>646<th>9</th><td>US-10-121-746-10</td><td>Sequence 10, Appl1</td></td>	6.4	646 <th>9</th> <td>US-10-121-746-10</td> <td>Sequence 10, Appl1</td>	9	US-10-121-746-10	Sequence 10, Appl1
	43	123.5 <th>6.0</th> <td>223<th>9</th><td>US-09-875-321-9</td><td>Sequence 9, Appl1</td></td>	6.0	223 <th>9</th> <td>US-09-875-321-9</td> <td>Sequence 9, Appl1</td>	9	US-09-875-321-9	Sequence 9, Appl1
	44	123.5 <th>6.0</th> <td>223<th>9</th><td>US-10-162-012-9</td><td>Sequence 9, Appl1</td></td>	6.0	223 <th>9</th> <td>US-10-162-012-9</td> <td>Sequence 9, Appl1</td>	9	US-10-162-012-9	Sequence 9, Appl1
	45	118 <th>5.8</th> <td>988<th>9</th><td>US-09-875-321-12</td><td>Sequence 12, Appl1</td></td>	5.8	988 <th>9</th> <td>US-09-875-321-12</td> <td>Sequence 12, Appl1</td>	9	US-09-875-321-12	Sequence 12, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-939-484-4  
Sequence 4, Application US/09939484  
Patent No. US20020032322A1  
GENERAL INFORMATION:  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lesage, Florian  
APPLICANT: Fink, Michel  
APPLICANT: Lazdunski, Michel  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
FILE REFERENCE: 1201-CIP-DIV-00  
CURRENT APPLICATION NUMBER: US/09/939,484  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 09/144,914  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 08/749,816  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/095,234  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: FR 96/01565  
PRIOR FILING DATE: 1996-02-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 394  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: TASK  
US-09-939-484-4  
Query Match 100.0%; Score 2042; DB 10; Length 394;  
Best Local Similarity 100.0%; Pred. No. 2e-182;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 MKRONVRLTALIVCTFTYLLGCAVFDALSEPELIERQRLERLQOELRARNINSOGYE 60  
DB 1 MKRONVRLTALIVCTFTYLLGCAVFDALSEPELIERQRLERLQOELRARNINSOGYE 60  
CY 61 ELERVRLRKHKGVGVRFAVSFYATVTTTGYGHAAPSTGCKVCFYALGIPL 120

Db 61 ELERVVLRKPKHAGVQMRPAGSFYFAITVITTTIGGHAAPSTDGCKVFCMFYALGIPL 120  
QY 121 TLVWFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
Db 121 TLVWFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTTIGFGDYVALOKDQALQTOPQVAFSFYIILTGLTVIGAFIN 240  
Db 181 YEHMTFFQAYYYCFITLTTIGFGDYVALOKDQALQTOPQVAFSFYIILTGLTVIGAFIN 240  
QY 241 LVVLRMTNMADEKDAEHRALLTRNGOAGGGGGSAAHTTDTASTAAAGGGGRNRY 300  
Db 241 LVVLRMTNMADEKDAEHRALLTRNGOAGGGGGSAAHTTDTASTAAAGGGGRNRY 300  
QY 301 AEVLHFOQSMCSCIMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
Db 301 AEVLHFOQSMCSCIMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
QY 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394  
Db 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 2  
US-09-939-483-4  
Sequence 4, Application US/09939483  
Patent No. US20020094558A1  
GENERAL INFORMATION:  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lesage, Florian  
APPLICANT: Fluk, Michel  
APPLICANT: Lazdunski, Michel  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
FILE REFERENCE: 1201-CIP-DIV-2-00  
CURRENT APPLICATION NUMBER: US/09/939,483  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 09/144,914  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 08/749,816  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: 60/095,234  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: FR 96/01565  
PRIOR FILING DATE: 1996-02-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 4  
LENGTH: 394  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: TASK  
US-09-939-483-4

Query Match 100.0%; Score 2042; DB 10; Length 394;  
Best Local Similarity 100.0%; Pred. No. 2e-182;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVRLTALVCTFTYLLVGAAPDALESEBELERORLELROELRARNVLSGGYE 60  
Db 1 MKRONVRLTALVCTFTYLLVGAAPDALESEBELERORLELROELRARNVLSGGYE 60  
QY 61 ELERVVLRKPKHAGVQMRPAGSFYFAITVITTTIGGHAAPSTDGCKVFCMFYALGIPL 120  
Db 61 ELERVVLRKPKHAGVQMRPAGSFYFAITVITTTIGGHAAPSTDGCKVFCMFYALGIPL 120  
QY 121 TLVWFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
Db 121 TLVWFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTTIGFGDYVALOKDQALQTOPQVAFSFYIILTGLTVIGAFIN 240  
Db 181 YEHMTFFQAYYYCFITLTTIGFGDYVALOKDQALQTOPQVAFSFYIILTGLTVIGAFIN 240

Db 181 YEHMTFFQAYYYCFITLTTIGFGDYVALOKDQALQTOPQVAFSFYIILTGLTVIGAFIN 240  
QY 241 LVVLRMTNMADEKDAEHRALLTRNGOAGGGGGSAAHTTDTASTAAAGGGGRNRY 300  
Db 241 LVVLRMTNMADEKDAEHRALLTRNGOAGGGGGSAAHTTDTASTAAAGGGGRNRY 300  
QY 301 AEVLHFOQSMCSCIMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
Db 301 AEVLHFOQSMCSCIMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
QY 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394  
Db 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 3  
US-09-798-584-15  
Sequence 15, Application US/09798584  
Patent No. US20020102676A1  
GENERAL INFORMATION:  
APPLICANT: Mu, David  
APPLICANT: Powers, Scott  
APPLICANT: Tularik Inc.  
TITLE OF INVENTION: KCNB: A NO. US20020102676A1 Potassium Channel Protein  
FILE REFERENCE: 018781-004010US  
CURRENT APPLICATION NUMBER: US/09/798,584  
CURRENT FILING DATE: 2001-03-03  
PRIOR APPLICATION NUMBER: US 60/186,951  
PRIOR FILING DATE: 2000-03-03  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 15  
LENGTH: 394  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human potassium channel KCNK3 (TASK1)  
US-09-798-584-15

Query Match 100.0%; Score 2042; DB 10; Length 394;  
Best Local Similarity 100.0%; Pred. No. 2e-182;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKRONVRLTALVCTFTYLLVGAAPDALESEBELERORLELROELRARNVLSGGYE 60  
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Db 61 ELERVVLRKPKHAGVQMRPAGSFYFAITVITTTIGGHAAPSTDGCKVFCMFYALGIPL 120  
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Db 121 TLVWFOSLGERINTLVRYLLHRAKKGLGMRADVSANNVLLIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTTIGFGDYVALOKDQALQTOPQVAFSFYIILTGLTVIGAFIN 240  
Db 181 YEHMTFFQAYYYCFITLTTIGFGDYVALOKDQALQTOPQVAFSFYIILTGLTVIGAFIN 240  
QY 241 LVVLRMTNMADEKDAEHRALLTRNGOAGGGGGSAAHTTDTASTAAAGGGGRNRY 300  
Db 241 LVVLRMTNMADEKDAEHRALLTRNGOAGGGGGSAAHTTDTASTAAAGGGGRNRY 300  
QY 301 AEVLHFOQSMCSCIMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
Db 301 AEVLHFOQSMCSCIMYKSREKLOYISIPMIIPROLDSTDTCVEQSHSPGGGGRYSDTPSR 360  
QY 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394  
Db 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 4

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US-09-939-484-5
; Sequence 5, Application US/09939484
; Patent No. US20020032322A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-484-5

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Query Match      89.1%; Score 1819; DB 10; Length 405;
Best Local Similarity 88.1%; Pred. No. 1,4e-161;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

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QY 4 QNVTLLALIVCTFTYLLVGAAVDALESEPELIERORLELROELRARNYLSGGYELE 63
DB 1 ENVTLLALIVCTFTYLLVGAAVDALESEPELIERORLELROELRARNYLSGGYELE 60
QY 64 RVLRLKPKHAGVQWRAGSFYFAITVITTTIGYHAPSTDGKVFPCMFALLGIPLTIV 123
DB 61 RVLRLKPKHAGVQWRAGSFYFAITVITTTIGYHAPSTDGKVFPCMFALLGIPLTIV 120
QY 124 MFSLSGERINTLVYLLHRAKKGIMRADYMANVYLIGFSCISTLCIGAAAFSYHER 183
DB 121 MFSLSGERINTLVYLLHRAKKGIMRADYMANVYLIGFSCISTLCIGAAAFSYHER 180
QY 184 WTEFOAYYYCFITLTITGFDYVALQKDALQTOPQYVAFSFYIILGLTVIGAFNLVY 243
DB 181 WTEFOAYYYCFITLTITGFDYVALQKDALQTOPQYVAFSFYIILGLTVIGAFNLVY 240
QY 244 LRFMTMAEEDKDAEHRALLTRNGAGGGG-----GSAHTTDTASTAA----- 291
DB 241 LRFMTMAEEDKDAEHRALLTRNGAGGGG-----GSAHTTDTASTAA----- 291
QY 292 --GGGFRNYYAEVLAHFOQSCCLMYKSRKLOYISIPMIIPROLDSTSDTCVEQSHSSPG 349
DB 301 GVGSGFRNYYAEVLAHFOQSCCLMYKSRKLOYISIPMIIPROLDSTSDTCVEHSHSSPG 360
QY 350 GGRYSPTPSRRLCSCGAPRSATSSVTGLHSLSTFRGLMKRRSSV 394
DB 361 GGRYSPTPSRRLCSCGAPRSATSSVTGLHSLSTFRGLMKRRSSV 405

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RESULT 5
US-09-939-483-5
; Sequence 5, Application US/09939483
; Patent No. US20020094558A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel

```

```

; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-483-5

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Query Match      89.1%; Score 1819; DB 10; Length 405;
Best Local Similarity 88.1%; Pred. No. 1,4e-161;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

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QY 4 QNVTLLALIVCTFTYLLVGAAVDALESEPELIERORLELROELRARNYLSGGYELE 63
DB 1 ENVTLLALIVCTFTYLLVGAAVDALESEPELIERORLELROELRARNYLSGGYELE 60
QY 64 RVLRLKPKHAGVQWRAGSFYFAITVITTTIGYHAPSTDGKVFPCMFALLGIPLTIV 123
DB 61 RVLRLKPKHAGVQWRAGSFYFAITVITTTIGYHAPSTDGKVFPCMFALLGIPLTIV 120
QY 124 MFSLSGERINTLVYLLHRAKKGIMRADYMANVYLIGFSCISTLCIGAAAFSYHER 183
DB 121 MFSLSGERINTLVYLLHRAKKGIMRADYMANVYLIGFSCISTLCIGAAAFSYHER 180
QY 184 WTEFOAYYYCFITLTITGFDYVALQKDALQTOPQYVAFSFYIILGLTVIGAFNLVY 243
DB 181 WTEFOAYYYCFITLTITGFDYVALQKDALQTOPQYVAFSFYIILGLTVIGAFNLVY 240
QY 244 LRFMTMAEEDKDAEHRALLTRNGAGGGG-----GSAHTTDTASTAA----- 291
DB 241 LRFMTMAEEDKDAEHRALLTRNGAGGGG-----GSAHTTDTASTAA----- 291
QY 292 --GGGFRNYYAEVLAHFOQSCCLMYKSRKLOYISIPMIIPROLDSTSDTCVEQSHSSPG 349
DB 301 GVGSGFRNYYAEVLAHFOQSCCLMYKSRKLOYISIPMIIPROLDSTSDTCVEHSHSSPG 360
QY 350 GGRYSPTPSRRLCSCGAPRSATSSVTGLHSLSTFRGLMKRRSSV 394
DB 361 GGRYSPTPSRRLCSCGAPRSATSSVTGLHSLSTFRGLMKRRSSV 405

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RESULT 6
US-09-746-491-61
; Sequence 61, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: NO. US20020137202A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 61
; LENGTH: 258
; TYPE: PRT

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ORGANISM: Mus musculus  
US-09-746-491-61

Query Match Best Local Similarity 96.1%; Pred. No. 2.5e-111;  
Matches 248; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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DB 1 MKRONVRLALIVCTFTYLLVGAADFDALESEBELIERORLEROELRARNYLSOGYE 60  
QY 61 ELERVYLRKPKHAGVQWRFAGSFYFAITVITTTIGGHAAPSTDGKVFQMFYALGIP 120  
DB 61 ELERVYLRKPKHAGVQWRFAGSFYFAITVITTTIGGHAAPSTDGKVFQMFYALGIP 120  
QY 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANMNLIGFSCISTLCIGAAAFSH 180  
DB 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANMNLIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTITGFGDYVALQKDALQTOPQVAFSEFYIITGLTVIGAF 240  
DB 181 YEHMTFFQAYYYCFITLTITGFGDYVALQKDALQTOPQVAFSEFYIITGLTVIGAF 240  
QY 241 LVVLRMTNMADEKRD 258  
DB 241 LVVLRMTNMADEKRD 258

## RESULT 7

US-09-798-584-1  
Sequence 1, Application US/09798584  
Patent No. US20020102676a1

GENERAL INFORMATION:  
APPLICANT: Mu, David  
APPLICANT: Powers, Scott  
APPLICANT: Tularik Inc.  
TITLE OF INVENTION: KCNB: A No. US20020102676a1e1 Potassium Channel Protein  
FILE REFERENCE: 018781-00401005  
CURRENT APPLICATION NUMBER: US/09/798,584  
CURRENT FILING DATE: 2001-03-03  
PRIOR APPLICATION NUMBER: US 60/186,951  
PRIOR FILING DATE: 2000-03-03  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 374  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human KCNB (Potassium Channel expressed in Breast)  
US-09-798-584-1

Query Match Best Local Similarity 54.7%; Score 1116; DB 10; Length 374;  
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

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DB 1 MKRONVRLALIVCTFTYLLVGAADFDALESEBELIERORLEROELRARNYLSOGYE 60  
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DB 61 ELERVYLRKPKHAGVQWRFAGSFYFAITVITTTIGGHAAPSTDGKVFQMFYALGIP 120  
QY 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANMNLIGFSCISTLCIGAAAFSH 180  
DB 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANMNLIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTITGFGDYVALQKDALQTOPQVAFSEFYIITGLTVIGAF 240  
DB 181 YEHMTFFQAYYYCFITLTITGFGDYVALQKDALQTOPQVAFSEFYIITGLTVIGAF 240  
QY 241 LVVLRMTNMADEKRD 258  
DB 241 LVVLRMTNMADEKRD 258

DB 241 LVVLRMTNMADEKRD 258  
QY 301 AEVLHQSVCGLWKKSRKLOYSIPMLIPRLSDTCVBOSSHSPGGGRYSDPPSR 359  
DB 287 KADVPDQVSCVCTYRSOD--YGRSVAPQSFSAKLAPHYHSHSYIEIESTLK 343  
QY 360 RCLCSGAPRSASISVSTGLHSLSTFRGLMKRRSSV 394  
DB 344 NSLFP---SPISISPGLSHSPFDHQLMKRRSV 374

## RESULT 8

US-09-746-491-60  
Sequence 60, Application US/09746491  
Patent No. US20020137202a1

GENERAL INFORMATION:  
APPLICANT: Burgess, Catherine E.  
TITLE OF INVENTION: No. US20020137202a1e1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 15966-621  
CURRENT APPLICATION NUMBER: US/09/746,491  
CURRENT FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: USSN 60/171,329  
PRIOR FILING DATE: 1999-12-21  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 60  
LENGTH: 365  
TYPE: PRT  
ORGANISM: Cavia porcellus  
US-09-746-491-60

Query Match Best Local Similarity 52.4%; Score 1069.5; DB 10; Length 365;  
Matches 226; Conservative 43; Mismatches 94; Indels 33; Gaps 6;

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DB 1 MKRONVRLALIVCTFTYLLVGAADFDALESEBELIERORLEROELRARNYLSOGYE 60  
QY 61 ELERVYLRKPKHAGVQWRFAGSFYFAITVITTTIGGHAAPSTDGKVFQMFYALGIP 120  
DB 61 ELERVYLRKPKHAGVQWRFAGSFYFAITVITTTIGGHAAPSTDGKVFQMFYALGIP 120  
QY 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANMNLIGFSCISTLCIGAAAFSH 180  
DB 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSANMNLIGFSCISTLCIGAAAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTITGFGDYVALQKDALQTOPQVAFSEFYIITGLTVIGAF 240  
DB 181 YEHMTFFQAYYYCFITLTITGFGDYVALQKDALQTOPQVAFSEFYIITGLTVIGAF 240  
QY 241 LVVLRMTNMADEKRD 258  
DB 241 LVVLRMTNMADEKRD 258  
QY 299 VVAEVLHQSVCGLWKKSRKLOYSIPMLIPRLSDTCVBOSSHSPGGGRYSDPPSR 358  
DB 292 -----DLQSVGCACATYRSP--QNGGATLAPPLHSHISGRLEI-----SPS 331  
QY 359 RCLCSGAPRSASISVSTGLHSLSTFRGLMKRRSSV 394  
DB 332 --TLKNSLFPSPISVSPGLHSPGDHRLMLRKS 365

## RESULT 9

US-09-746-491-59  
Sequence 59, Application US/09746491  
Patent No. US20020137202a1

GENERAL INFORMATION:  
APPLICANT: Burgess, Catherine E.  
TITLE OF INVENTION: No. US20020137202a1e1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 15966-621

[illegible][illegible]

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RESULT 12
US-09-864-761-34389
: Sequence 34389, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharron G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Weisheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Aecmlca X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23

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Best Local Similarity	31.6%	Pred. No. 2.5e-26;		
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RESULT 15  
US-09-828-746-6

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000001 Sequence 6, Application No./09/828746
000002 Patent No. US20020028485A1
000003 GENERAL INFORMATION:
000004 APPLICANT: Helen Jane Meadows
000005 APPLICANT: Conrad Gerald Chapman
000006 TITLE OF INVENTION: NOVEL CHEMOCARD
000007 FILE REFERENCE: GP-30031-ID
000008 CURRENT APPLICATION NUMBER: US/09/828,746
000009 CURRENT FILING DATE: 2001-04-09
000010 PRIOR APPLICATION NUMBER: US 09/236,080
000011 PRIOR FILING DATE: 1999-01-25
000012 PRIOR APPLICATION NUMBER: EP 98300570.3
000013 PRIOR FILING DATE: 1998-01-27
000014 PRIOR APPLICATION NUMBER: UK 9822135.1
000015 PRIOR FILING DATE: 1998-10-09
000016 NUMBER OF SEQ ID NOS: 6
000017 SOFTWARE: FastSeq for Windows Version 3.0
000018 SEQ ID NO 6
000019 LENGTH: 411
000020 TYPE: prt

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Best Local Similarity	31.6%	Pred. No.	3.6e-26				
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						Gaps	9

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Job time : 27 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 15:11:12 : Search time 72 Seconds

(Without alignments)  
729.177 Million cell updates/sec

Title: US-09-939-484-4

Perfect score: 2042  
Sequence: 1 MKRONVRLTALIVCTFTYLL.....STGLHSLSFRGLMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	2042	100.0	394	21	AAE10343
2	2042	100.0	394	21	AAV79674
3	2042	100.0	394	21	AAV87291
4	1819	89.1	405	21	AAV95230
5	1235.5	60.5	309	22	AAU07620
6	1116	54.7	374	21	AAAB18807
7	1116	54.7	374	21	AAAB18813
8	1116	54.7	374	22	AAAG3938
9	1116	54.7	374	23	AAE22969
10	1116	54.7	374	23	AAE13279

11	846	41.4	400	22	AAE10679
12	838	41.0	330	22	AAAB47334
13	838	41.0	400	22	AAE10678
14	838	41.0	400	23	AAE13286
15	785.5	38.5	436	22	ABG29273
16	777	38.1	340	22	ABG64375
17	774	37.9	279	22	ABG28454
18	774	37.9	279	22	ABG3636
19	774	37.9	279	22	ABG19091
20	774	37.9	279	22	AAAB4409
21	774	37.9	279	22	AAAB6810
22	774	37.9	279	22	AAAB4676
23	774	37.9	279	22	AAAB7095
24	774	37.9	279	22	AAAB2399
25	774	37.9	279	22	ABG36465
26	773	37.9	408	22	AAAB1804
27	742	36.3	398	22	ABG1787
28	379	18.6	361	22	AAAB1805
29	370	18.1	411	21	AAE10342
30	369	18.1	370	20	AAV30648
31	369	18.1	411	20	AAV28497
32	366.5	17.9	295	23	AAE21164
33	364	17.8	426	22	AAU07618
34	363	17.8	411	20	AAV34133
35	363	17.8	411	20	AAV28496
36	363	17.8	411	21	AAE10341
37	363	17.8	411	22	AAAB5004
38	362	17.7	292	23	AAU09893
39	362	17.7	292	23	AAU09892
40	361	17.7	294	23	AAU09892
41	360	17.6	426	22	AAU07622
42	359	17.6	426	22	AAU07623
43	358	17.5	534	23	AAU01355
44	356	17.4	426	22	AAU07625
45	355	17.4	411	23	AAE16597

#### ALIGNMENTS

RESULT 1  
AAE10343  
AAE10343 standard; Protein: 394 AA.

AC AAE10343;  
DT 10-DEC-2001 (first entry)  
XX Murine TASK potassium channel protein.  
DE Murine TASK potassium channel protein.  
XX Murine: potassium channel protein; TREK-1; TASK: anaesthetic; analgesia;  
KW amesla.  
XX Mus sp.  
XX WO200047738-A2.  
XX 17-AUG-2000.  
XX 11-FEB-2000; 2000WO-IB00226.  
XX 12-FEB-1999; 99US-0119727.  
XX 11-FEB-2000; 2000US-0503069.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;  
XX WPI: 2000-549146/50.  
XX Novel nucleic acid encoding a TREK-1 potassium channel protein for  
XX transfecting cells to be used to identify compounds with anesthetic  
XX properties -

XX Claim 23: Page 34-35; 39pp; English.

PS The invention relates to human and mouse TREK-1 potassium channel

XX proteins and their corresponding DNA molecules. TREK-1 nucleic acid is

CC useful for transfecting cells to induce expression of the TREK-1

CC potassium channel protein. These cells are then used in assays to

CC identify compounds which have anaesthetic properties, producing a safe,

CC reversible state of unconsciousness with concurrent amnesia and analgesia

CC in a mammal upon inhalation. The present sequence is murine TASK

CC potassium channel protein related to the invention.

XX

SO Sequence 394 AA:

Query Match 100.0%; Score 2042; DB 21; Length 394;

Best Local Similarity 100.0%; Pred. No. 7.8e-214;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONRTALIVCTFTYLLVGAAVDALESEPELIERORLELROELRARNYLSGGYE 60

DB 1 MKRONRTALIVCTFTYLLVGAAVDALESEPELIERORLELROELRARNYLSGGYE 60

QY 61 ELERVYLRLKPKHAGVOMRAGSFYFAIVYITTTIGYGHAASTDGKVKFCMFYALLGIP 120

DB 61 ELERVYLRLKPKHAGVOMRAGSFYFAIVYITTTIGYGHAASTDGKVKFCMFYALLGIP 120

QY 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSNANVYLIGFSCISTLCIGAAAFSH 180

DB 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSNANVYLIGFSCISTLCIGAAAFSH 180

QY 181 YEHWTFQAYYYCFITLTITGEGDYVALOKDQLQPOPVAFSFYIITGLTVIGAFIN 240

DB 181 YEHWTFQAYYYCFITLTITGEGDYVALOKDQLQPOPVAFSFYIITGLTVIGAFIN 240

QY 241 LVVLRMTNNAEDERDAERHALLTRNGAGGGGSAHTTDTASTAAAGGGRFNNY 300

DB 241 LVVLRMTNNAEDERDAERHALLTRNGAGGGGSAHTTDTASTAAAGGGRFNNY 300

QY 301 AEVLHFOQSMCSCIWYSREKLOYSIPIIPRDLSTDCVEQSHSPGGGGRYSDTPSR 360

DB 301 AEVLHFOQSMCSCIWYSREKLOYSIPIIPRDLSTDCVEQSHSPGGGGRYSDTPSR 360

QY 361 CIGSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394

DB 361 CIGSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394

RESULT 2

AAV79674

ID AAV79674 standard; Protein; 394 AA.

AC AAV79674;

DT 29-AUG-2000 (first entry)

XX

DE Human potassium channel TASK1.

KW TASK1: TWIK-related acid-sensitive K+ channel 1; human;

KW potassium channel; drug screening; hypertension;

KW hypotensive; epilepsy; arrhythmia; vascular diseases;

KW neurodegenerative disease; ischemia; anoxia; endocrine disease;

KW muscle disease; therapy.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Modified-site 53

FT Modified-site /note= "n-glycosylated"

FT Modified-site 323

FT Modified-site /note= "O-phosphorylated"

FT Modified-site 383

FT Modified-site /note= "O-phosphorylated"

FT Modified-site 392

FT /note= "O-phosphorylated"

FT Modified-site 393

FT /note= "O-phosphorylated"

XX

XX WO200027871-A2.

XX

XX 18-MAY-2000.

XX

XX 09-NOV-1999; 99MO-IB01886.

XX

XX 09-NOV-1998; 98US-0107692.

XX 08-NOV-1999; 99US-0436265.

XX

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Duprat F, Lesage F, Lazdunski M;

XX N-PSDB; AAA27746.

DR WPI; 2000-376487/32.

DR

XX

PT New nucleic acid encoding a non-inactivating outwardly rectifying

PT potassium transport channel, designated TASK2, useful in the treatment

PT of hypertension or dysfunctions of the kidney, liver or pancreas -

PS Disclosure; Fig 8; 91pp; English.

XX

XX The present sequence is that of human TASK1 (TWIK-related

XX acid-sensitive K+ channel), a member of a new family of 2P

XX domain potassium channels, also including TWIK-1 (see AAV79673) and

XX novel TASK2 (see AAV79675). TASK1 is expressed in many different

XX tissues, and at particularly high levels in pancreas and placenta.

XX Host cells expressing TWIK-1 family members can be used to screen

XX for substances that modulate the activity of members of the TWIK-1

XX family of potassium channels. The drugs identified may be

XX useful in the treatment of diseases of the heart or of the nervous

XX system, such as epilepsy, arrhythmia, vascular diseases,

XX neurodegenerative diseases, kidney, liver or pancreas diseases,

XX hypertension, diseases associated with ischaemia or anoxia,

XX endocrine diseases associated with anomalies of hormone secretion,

XX and muscle diseases.

XX

SO Sequence 394 AA:

Query Match 100.0%; Score 2042; DB 21; Length 394;

Best Local Similarity 100.0%; Pred. No. 7.8e-214;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONRTALIVCTFTYLLVGAAVDALESEPELIERORLELROELRARNYLSGGYE 60

DB 1 MKRONRTALIVCTFTYLLVGAAVDALESEPELIERORLELROELRARNYLSGGYE 60

QY 61 ELERVYLRLKPKHAGVOMRAGSFYFAIVYITTTIGYGHAASTDGKVKFCMFYALLGIP 120

DB 61 ELERVYLRLKPKHAGVOMRAGSFYFAIVYITTTIGYGHAASTDGKVKFCMFYALLGIP 120

QY 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSNANVYLIGFSCISTLCIGAAAFSH 180

DB 121 TLVMPQSLGERINTLVRYLLHRAKKGIGMRADVSNANVYLIGFSCISTLCIGAAAFSH 180

QY 181 YEHWTFQAYYYCFITLTITGEGDYVALOKDQLQPOPVAFSFYIITGLTVIGAFIN 240

DB 181 YEHWTFQAYYYCFITLTITGEGDYVALOKDQLQPOPVAFSFYIITGLTVIGAFIN 240

QY 241 LVVLRMTNNAEDERDAERHALLTRNGAGGGGSAHTTDTASTAAAGGGRFNNY 300

DB 241 LVVLRMTNNAEDERDAERHALLTRNGAGGGGSAHTTDTASTAAAGGGRFNNY 300

QY 301 AEVLHFOQSMCSCIWYSREKLOYSIPIIPRDLSTDCVEQSHSPGGGGRYSDTPSR 360

DB 301 AEVLHFOQSMCSCIWYSREKLOYSIPIIPRDLSTDCVEQSHSPGGGGRYSDTPSR 360

QY 361 CIGSGAPRAISSVSTGLSLSTFRGLMKRRSSV 394



DB 361 CLC GAPRAISSVSTGLHSLSTRGLMKRRSSV 394

RESULT 3  
AAV87291  
ID AAV87291 standard; Protein: 394 AA.  
XX  
AC AAV87291;  
XX  
DT 11-MAY-2000 (first entry)  
XX  
DE Human signal peptide containing protein HSP68 SEQ ID NO:68.  
XX  
KW Human: signal peptide-containing protein; HSP; diagnosis; cancer;  
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
KW anti-infective; neuroprotective; cardiovascular; hepatotropic;  
KW antidiabetic; gene therapy; cell proliferation; neurological disorder;  
KW reproductive disorder; developmental disorder; arteriosclerosis;  
KW cleftosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
KW Parkinson's disease; Huntington's disease; ovulatory defect;  
KW muscular dystrophy.  
XX  
OS Homo sapiens.  
XX  
PN NC0200000610-A2.  
XX  
PD 06-JAN-2000.  
XX  
PE 25-JUN-1999; 99MO-US14484.  
XX  
PR 26-JUN-1998; 98US-0090762.  
PR 31-JUL-1998; 98US-0094983.  
PR 01-OCT-1998; 98US-0102686.  
PR 11-DEC-1998; 98US-0112129.  
XX  
XX  
PA (INCY- ) INCYTE PHARM INC.  
PI Lal P. Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
PI Aberblom IE, Au-young J, Yue H, Patterson C, Reddy R, Hillman JL;  
PI Bandman O;  
XX  
XX  
DR MPI: 2000-160673/14.  
DR N-PSDB: AAZ98176.  
XX  
XX  
PT New human signal peptide-containing proteins useful in treatment,  
PT prevention and diagnosis of e.g. cancer, inflammation and  
PT cardiovascular disease  
XX  
XX  
PS (claim 1; Page 207-208; 327pp; English.  
XX  
XX  
AAZ98109 to AAZ98242 encode AAV87224 to AAV87357 which represent the  
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
CC neuroprotective, cardiovascular and antidiabetic activities, and can  
CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSP. Antagonists of  
CC HSP are used to treat or prevent disorders associated with increased  
CC activity or function of HSP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases), schizophrenia, ovulatory defects, muscular dystrophy). HSP  
CC nucleic acids can be used for the recombinant production of HSP, for  
CC detecting HSP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring). In gene therapy, as antisense,  
CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
CC or genetic variations, and for chromosomal mapping. HSP are also used to  
CC raise specific antibodies (Ab) and to screen for agonists and  
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic

CC antagonists, in competitive drug screens, and for purification of HSP  
CC from natural sources.  
XX  
XX  
SO Sequence 394 AA;  
Query Match 100.0%; Score 2042; DB 21; Length 394;  
Best Local Similarity 100.0%; Pred. No. 7.8e-214;  
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCTFTYLLVGAAPDALESEPELIERORLELROQELRARNYNSOGYE 60  
DB 1 MKRONVRLALIVCTFTYLLVGAAPDALESEPELIERORLELROQELRARNYNSOGYE 60  
QY 61 ELEHVYLRKPKKAGVOMRFGSFYFAITVTTTGYHAPSTGKVFYLLGIPL 120  
DB 61 ELEHVYLRKPKKAGVOMRFGSFYFAITVTTTGYHAPSTGKVFYLLGIPL 120  
QY 121 TLVVFOSIGERINTLVRLHRAKKGIMRADVSMANMVLIGFSCISTICGAAAFSH 180  
DB 121 TLVVFOSIGERINTLVRLHRAKKGIMRADVSMANMVLIGFSCISTICGAAAFSH 180  
QY 181 YEHWTFQAYYYCEITLTITIGFDYVALQKDOALQTOPYVAFSVYILTGLYIGAFLN 240  
DB 181 YEHWTFQAYYYCEITLTITIGFDYVALQKDOALQTOPYVAFSVYILTGLYIGAFLN 240  
QY 241 LVYLRFTMTNAEDKRDRAEHRALLTRNGQAGGGGSAHTTDRASSTAAAGGCFRNVY 300  
DB 241 LVYLRFTMTNAEDKRDRAEHRALLTRNGQAGGGGSAHTTDRASSTAAAGGCFRNVY 300  
QY 301 AEVLHFOGMCCLWYKSKREKQYSIPMTIPRDLSTSPDCVQSHSPGCGGRYSPTPSRR 360  
DB 301 AEVLHFOGMCCLWYKSKREKQYSIPMTIPRDLSTSPDCVQSHSPGCGGRYSPTPSRR 360  
QY 361 CLC GAPRAISSVSTGLHSLSTRGLMKRRSSV 394  
DB 361 CLC GAPRAISSVSTGLHSLSTRGLMKRRSSV 394

RESULT 4  
AAV95230  
ID AAV95230 standard; Protein: 405 AA.  
XX  
XX  
AC AAV95230;  
XX  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Mouse potassium channel TASK.  
XX  
XX  
KW TASK: TWIK-related acid-sensitive K<sup>+</sup> channel; mouse;  
KW potassium channel; drug screening; hypertension;  
KW hypotensive; epilepsy; arrhythmia; vascular diseases;  
KW neurodegenerative disease; ischaemia; enoxia; endocrine disease;  
KW muscle disease; therapy.  
XX  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 50  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 334  
FT Modified-site /note= "O-phosphorylated"  
FT Modified-site 403  
FT Modified-site /note= "O-phosphorylated"  
FT Modified-site 404  
FT Modified-site /note= "O-phosphorylated"  
XX  
PN NC0200027871-A2.  
XX  
PD 18-MAY-2000.  
XX  
XX  
PF 09-NOV-1999; 99MO-IB01886.  
XX  
XX  
PR 09-NOV-1998; 98US-0107692.

PR 08-NOV-1999; 9905-0436265.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX Duprat F, Lesage F, Lazdunski M;  
XX WPI, 2000-376487/32.  
XX  
XX New nucleic acid encoding a non-inactivating outwardly rectifying  
PT potassium transport channel, designated TASK2, useful in the treatment  
PT of hypertension or dysfunctions of the kidney, liver or pancreas  
XX  
XX Disclosure; Fig 8; 91pp; English.  
XX  
XX The present sequence is that of murine TASK (TWIK-related  
CC acid-sensitive K<sup>+</sup> channel), a member of a new family of 2P  
CC domain potassium channels, also including human TWIK-1 (see  
CC AAY79673), human TASK1 (see AAY79674) and novel human TASK2 (see  
CC AAY79673). Human and mouse TASK proteins share 85% identity,  
CC indicating that they are products of orthologous genes. Host  
CC cells expressing TWIK-1 family members can be used to screen  
CC for substances that modulate the activity of members of the TWIK-1  
CC family of potassium channels. The drugs identified may be  
CC useful in the treatment of diseases of the heart or of the nervous  
CC system, such as epilepsy, arrhythmia, vascular diseases,  
CC neurodegenerative diseases, kidney, liver or pancreas diseases,  
CC hypertension, diseases associated with ischaemia or anoxia,  
CC endocrine diseases associated with anomalies of hormone secretion,  
CC and muscle diseases.  
XX  
XX Sequence 405 AA:  
SO  
Query Match 89.1%; Score 1819; DB 21; Length 405;  
Best Local Similarity 88.1%; Pred. No. 1.8e-189;  
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;  
QY 4 QNVRTALIVCTFTYLLVGAAYVDALSEPELIERORLELROELRARNYLSGGYEEL 63  
DB 1 ENVRTALIVCTFTYLLVGAAYVDALSEPELIERORLELROELRARNYLSGGYEEL 60  
QY 64 RVLRLKPKHAGYQVMPFAGSFYPAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 123  
DB 61 RVLRLKPKHAGYQVMPFAGSFYPAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 120  
QY 124 MFQSLGERINTLVRYLLHRAKKGGMRRADVSANNAVLLGFSCISTLTGGAASFHYEH 183  
DB 121 MFQSLGERINTLVRYLLHRAKKGGMRRADVSANNAVLLGFSCISTLTGGAASFHYEH 180  
QY 184 WFFFOAYVYCFITLTITIGFDYVALOKDQALOTOPQYVAFSFIYLLTGLTVIGAFNLVY 243  
DB 181 WFFFOAYVYCFITLTITIGFDYVALOKDQALOTOPQYVAFSFIYLLTGLTVIGAFNLVY 240  
QY 244 LRFMTNNAEDEKRAHRRALLTHNGQAVGLGSLCSLSGIDVPRDPYTCALAAAGVGV 300  
DB 241 LRFMTNNAEDEKRAHRRALLTHNGQAVGLGSLCSLSGIDVPRDPYTCALAAAGVGV 300  
QY 292 --GGGFRNVVAEVLHFGSMCSCLYKSKREKLYSIPMIIIPDLSTSDTCVEQSHSPG 349  
DB 301 GVGSGSFRNVVAEVLHFGSMCSCLYKSKREKLYSIPMIIIPDLSTSDTCVEHSHSPG 360  
QY 350 GGRYSPTSPSRRCSCGAPRSATISSVSTGLHSLSTFGMLKRRSSV 394  
DB 361 GGRYSPTSPSRRCSCGAPRSATISSVSTGLHSLSTFGMLKRRSSV 405

## RESULT 5

AAU07620 standard; Protein; 309 AA.  
ID AAU07620  
XX  
XX AAU07620;  
XX  
XX  
DT 21-NOV-2001 (first entry)  
XX

DE Mouse 2P channel protein #1.  
XX Transmembrane potassium ion channel protein; inward potassium flux;  
XX pest control; membrane potential; pesticide; antihelminthic; nematode;  
KW insect; 2P channel; mouse.  
XX  
XX Mus musculus.  
XX WO200161006-A2.  
XX  
XX 23-AUG-2001.  
XX  
XX 14-FEB-2001; 2001MO-US04680.  
XX  
XX 15-FEB-2000; 2000US-0503849.  
XX  
XX (BADI ) BASF CORP.  
XX  
XX Pausch MH;  
XX WPI; 2001-536570/59.  
XX N-PSDB; AAS12179.  
XX  
XX New polypeptide, a mutant potassium ion channel protein for improving  
PT inward potassium flux under acidic conditions  
XX  
XX Example 18; Page 53; 131pp; English.  
XX  
XX The invention relates to a mutant potassium ion channel protein, having  
CC four membrane spanning domains and two pore forming domains, comprising a  
CC mutation at the second pore forming domain. The expression of the mutant  
CC protein in a cell confers improved inward potassium flux and the ability  
CC to grow in the presence of potassium. Mutant proteins and their  
CC corresponding polynucleotide sequences can therefore be used to improve  
CC inward potassium flux into cells under acidic conditions by modulating  
CC the membrane potential using therapeutic agents. The sequences may be  
CC used to develop agonists and antagonists of potassium channel proteins in  
CC order to control pests such as nematodes and insects. This sequence  
CC represents a mouse 2P channel protein.  
XX  
XX Sequence 309 AA:  
SO  
Query Match 60.5%; Score 1235.5; DB 22; Length 309;  
Best Local Similarity 83.9%; Pred. No. 5.9e-126;  
Matches 250; Conservative 8; Mismatches 27; Indels 13; Gaps 3;  
QY 4 QNVRTALIVCTFTYLLVGAAYVDALSEPELIERORLELROELRARNYLSGGYEEL 63  
DB 13 ENVRTALIVCTFTYLLVGAAYVDALSEPELIERORLELROELRARNYLSGGYEEL 72  
QY 64 RVLRLKPKHAGYQVMPFAGSFYPAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 123  
DB 73 RVLRLKPKHAGYQVMPFAGSFYPAITVITTTIGYGHAPSTDGKVCMEFYALLGIPLTLY 132  
QY 124 MFQSLGERINTLVRYLLHRAKKGGMRRADVSANNAVLLGFSCISTLTGGAASFHYEH 183  
DB 121 MFQSLGERINTLVRYLLHRAKKGGMRRADVSANNAVLLGFSCISTLTGGAASFHYEH 192  
QY 184 WFFFOAYVYCFITLTITIGFDYVALOKDQALOTOPQYVAFSFIYLLTGLTVIGAFNLVY 241  
DB 193 WFFFOAYVYCFITLTITIGFDYVALOKDQALOTOPQYVAFSFIYLLTGLTVIGAFNLVY 249  
QY 242 VVLRFTNNAEDEKRAHRRALLTHNGQAVGLGSLCSLSGIDVPRDPYTCALAA 307  
DB 250 VVLRFTNNAEDEKRAHRRALLTHNGQAVGLGSLCSLSGIDVPRDPYTCALAA 307

## RESULT 6

AAB18807 standard; Protein; 374 AA.  
ID AAB18807  
XX  
XX AAB18807;  
XX  
XX  
DT  
XX

DT 22-JAN-2001 (first entry)  
 XX Amino acid sequence of a human DKC1 polypeptide.  
 DE  
 XX Human: DKC1; potassium channel; cancer; pulmonary disease; depression;  
 KW cardiovascular disease; inflammatory disease; renal disease; pain;  
 KW psychiatric disorder; schizophrenia; neurodegenerative disease;  
 KW Alzheimer's disease; neurological disorder; migraine; epilepsy;  
 KW sleep-related disorder; erectile dysfunction; alopecia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200053628-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 02-MAR-2000; 2000WO-EP01750.  
 XX  
 PR 05-MAR-1999; 99GB-0005061.  
 PR 10-FEB-2000; 2000GB-0003112.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Duckworth DM, Godden RJ, Chapman CG, Meadows HJ;  
 DR WPI: 2000-587424/55.  
 DR N-PSDB: AAA75886.  
 XX  
 PT Polypeptides and polynucleotides of the potassium channel family,  
 PT useful for identifying agonists/antagonists of therapeutic use and  
 PT diagnosis and treatment of cancer, pulmonary, cardiovascular,  
 PT inflammatory and renal disease -  
 XX  
 PS Claim 1; Page 25; 36pp; English.  
 XX  
 CC The present sequence represents human DKC1 polypeptide. The polypeptide  
 CC is a member of the potassium channel family. The DKC1 polypeptides and  
 CC polynucleotides are useful for treating diseases including cancer,  
 CC pulmonary, cardiovascular, inflammatory or renal diseases, pain,  
 CC psychiatric disorders including depression and schizophrenia,  
 CC neurodegenerative disease including Alzheimer's, neurological disorders,  
 CC migraine, epilepsy, sleep-related disorders, erectile dysfunction and  
 CC alopecia. DKC1 polynucleotides are useful as diagnostic reagents for  
 CC detecting mutations in the associated gene.  
 CC  
 XX Sequence 374 AA:  
 SQ  
 Query Match 54.7%; Score 1116; DB 21; Length 374;  
 Best Local Similarity 59.0%; Pred. No. 8.7e-113;  
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;  
 QY 1 MKRONVRLALIVCTFTYLLVGAADFALSEPELIERQRLRQELRARNYNSGGYE 60  
 DB 1 MKRONVRLSLIVCTFTYLLVGAADFALSDHEEREKKAERIRKGYNTISSEDR 60  
 QY 61 ELEVRVRLKPKHKGAVQWRFGSFYFATVTTTIGYGAASSTGKVCFCFYALGTL 120  
 DB 61 QLELVYIQLSEPHRAGVQWKFAGSFYFATVTTTIGYGAAGTDAKGFCAFYAVLGTL 120  
 QY 121 TLVFOSLGERINTLVRLTHRAKKGGLMRADYSMMANVYIGFSCSTICIGAAFSH 180  
 DB 121 TLVFOSLGERINTLVRLTHRAKKGGLMRADYSMMANVYIGFSCSTICIGAAFSH 180  
 QY 181 YEHTTFOAYTYCTITLTGFGDYVALQKDALQTOPQVYAFSVYITGLVYIGAFLN 240  
 DB 181 CEESFPHAYTYCTITLTGFGDYVALQKDALQKPLVYAFSFMVTLVGLVYIGAFLN 240  
 QY 241 LVVLRFTMNADKRDKEHRAALLTRNGAGGGGGGSAHTTDAASSRAAGGGGFRVY 300  
 DB 241 LVVLRFTMNSEDEKRDKEHRAALLTRNGAGGGGGGSAHTTDAASSRAAGGGGFRVY 300  
 QY 301 -AEVLHQSCKMSCLMYKSREKLOYISPIIIPRDLSTSDPTCVESHSPPGGGGRYSDPTPSR 359  
 DB 301 -AEVLHQSCKMSCLMYKSREKLOYISPIIIPRDLSTSDPTCVESHSPPGGGGRYSDPTPSR 359

DB 287 KADVPDLQSCVCTCYRSQD---YGRSVAPDQNSPAKLADHPHISYKIEISPSTLK 343  
 QY 360 RCLCSGAPRAISSYVSTGLSLSTFRGLMKRRSSV 394  
 DB 344 NSLFP---SPISISPLSHSTHDQRLMKRRKRV 374  
 RESULT 7  
 AAB18813  
 ID AAB18813 standard; Protein; 374 AA.  
 AC AAB18813;  
 XX  
 XX 22-JAN-2001 (first entry)  
 DT  
 XX Protein encoded by an EST related to a human DKC1 cDNA.  
 DE  
 KW Human: DKC1; potassium channel; cancer; pulmonary disease; depression;  
 KW cardiovascular disease; inflammatory disease; renal disease; pain;  
 KW psychiatric disorder; schizophrenia; neurodegenerative disease;  
 KW Alzheimer's disease; neurological disorder; migraine; epilepsy;  
 KW sleep-related disorder; erectile dysfunction; alopecia;  
 KW expressed sequence tag; EST.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 PN MO200053628-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 02-MAR-2000; 2000WO-EP01750.  
 XX  
 PR 05-MAR-1999; 99GB-0005061.  
 PR 10-FEB-2000; 2000GB-0003112.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Duckworth DM, Godden RJ, Chapman CG, Meadows HJ;  
 DR WPI: 2000-587424/55.  
 DR N-PSDB: AAA75887.  
 XX  
 PT Polypeptides and polynucleotides of the potassium channel family,  
 PT useful for identifying agonists/antagonists of therapeutic use and  
 PT diagnosis and treatment of cancer, pulmonary, cardiovascular,  
 PT inflammatory and renal disease -  
 XX  
 PS Claim 12; Page 26; 36pp; English.  
 XX  
 CC The present sequence is encoded by an expressed sequence tag (EST) which  
 CC is related to a cDNA encoding a human DKC1 polypeptide. The polypeptide  
 CC is a member of the potassium channel family. The DKC1 polypeptides and  
 CC polynucleotides are useful for treating diseases including cancer,  
 CC pulmonary, cardiovascular, inflammatory or renal diseases, pain,  
 CC psychiatric disorders including depression and schizophrenia,  
 CC neurodegenerative disease including Alzheimer's, neurological disorders,  
 CC migraine, epilepsy, sleep-related disorders, erectile dysfunction and  
 CC alopecia. DKC1 polynucleotides are useful as diagnostic reagents for  
 CC detecting mutations in the associated gene.  
 CC  
 XX Sequence 374 AA:  
 SQ  
 Query Match 54.7%; Score 1116; DB 21; Length 374;  
 Best Local Similarity 59.0%; Pred. No. 8.7e-113;  
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;  
 QY 1 MKRONVRLALIVCTFTYLLVGAADFALSEPELIERQRLRQELRARNYNSGGYE 60  
 DB 1 MKRONVRLSLIVCTFTYLLVGAADFALSDHEEREKKAERIRKGYNTISSEDR 60  
 QY 61 ELEVRVRLKPKHKGAVQWRFGSFYFATVTTTIGYGAASSTGKVCFCFYALGTL 120  
 DB 61 QLELVYIQLSEPHRAGVQWKFAGSFYFATVTTTIGYGAAGTDAKGFCAFYAVLGTL 120



FT Modified-site 55..58 /note- "Casein kinase II phosphorylation site"  
 FT Region 80..96 /note- "P-loop"  
 FT Modified-site 102..107 /note- "N-myristoylation site"  
 FT Domain 108..125 /note- "Transmembrane domain 2"  
 FT Modified-site 117..122 /note- "N-myristoylation site"  
 FT Modified-site 127..130 /note- "Casein kinase II phosphorylation site"  
 FT Modified-site 148..153 /note- "N-myristoylation site"  
 FT Domain 159..178 /note- "Transmembrane domain 3"  
 FT Modified-site 179..182 /note- "Casein kinase II phosphorylation site"  
 FT Region 190..208 /note- "P-loop"  
 FT Domain 219..243 /note- "Transmembrane domain 4"  
 FT Modified-site 236..241 /note- "N-myristoylation site"  
 FT Modified-site 251..254 /note- "Casein kinase II phosphorylation site"  
 FT Modified-site 266..271 /note- "N-myristoylation site"  
 FT Modified-site 319..321 /note- "Protein kinase C phosphorylation site"  
 FT Modified-site 331..333 /note- "Protein kinase C phosphorylation site"  
 FT Modified-site 341..343 /note- "Protein kinase C phosphorylation site"  
 FT Modified-site 360..363 /note- "Casein kinase II phosphorylation site"  
 FT Modified-site 370..373 /note- "cAMP and cGMP dependent protein kinase phosphorylation site"  
 FT PN W0200226983-A2.  
 PD 04-APR-2002.  
 XX 25-SEP-2001; 2001MO-US30048.  
 XX 25-SEP-2000; 2000US-235059P.  
 PA (MILT-) MILLENNIUM PHARM INC.  
 XX  
 PI Curtis RAD;  
 XX  
 DR WPI: 2002-416481/44.  
 DR N-PSDB: AAD36247.  
 XX  
 PT New isolated human tandem of P domains in weak inward rectifying  
 PT potassium channel polypeptide, 56115, useful for treating central  
 PT nervous system, cardiovascular, pain, and cellular proliferation  
 PT disorders  
 XX  
 PS Claim 13; Fig 2; 99p; English.  
 XX  
 CC The invention relates to human tandem of P domains in a weak inward  
 CC rectifying potassium channel polypeptides (TWIK-9) termed 36115 and  
 CC nucleic acid molecules encoding such polypeptides. Sequences of the  
 CC invention are useful for treating TWIK-9-associated or related  
 CC disorders such as central nervous system disorders (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease), autonomic function  
 CC disorders (e.g., hypertension, sleep disorders, neuropsychiatric  
 CC disorders (e.g., depression, schizophrenia), learning or memory disorders  
 CC (e.g. amnesia), bipolar affective disorders, cardiac-related disorders  
 CC (e.g. arteriosclerosis, myocardial infarction), pain disorders, cellular  
 CC proliferation, growth, differentiation or migration disorders (e.g.

CC cancer) and disorders of tissues in which TWIK-9 protein is predominantly  
 CC expressed. They are also useful in screening assays, detection assays  
 CC (e.g. chromosomal mapping, tissue typing, forensic biology), predictive  
 CC medicine (e.g., diagnostic assays, prognostic assays, monitoring  
 CC clinical trials and pharmacogenomics) and in methods of treatment (e.g.  
 CC therapeutic and prophylactic). TWIK-9 polynucleotides are used in gene  
 CC therapy. The present sequence is human TWIK-9 protein.  
 XX  
 SQ Sequence 374 AA;  
 Query Match 54.7%; Score 116; DB 23; Length 374;  
 Best Local Similarity 59.0%; Pred. No. 8.7e-113;  
 Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;  
 QY 1 MKRONVRLALIVCTFFYLLVGAAPDALESEPELIERORLELROELRARNYLSQGYE 60  
 DB 1 MKRONVRLSLIVCTFFYLLVGAAPDALESDHEMREEEKLAKAEIRIKGYNISSEDEYR 60  
 QY 61 ELERVVRLKPKKAGVGMRFAGSFYFAITVTTTGYGHAAPSTPDGKGVFCFVALGIP 120  
 DB 61 QLELVILQSEPHRAGVGMKRFAGSFYFAITVTTTGYGHAAPSTPDGKGVFCFVALGIP 120  
 QY 121 TLVMEQSLGERINTLVRYLLHRKKGLGMRRADYSANMVLIGFSCISTLCIGAAFSH 180  
 DB 121 TLVMEQSLGERMNTFVRYLLKRIKCCGMRRITDVSMEWTVGPFSCMGFLCIGAAFSQ 180  
 QY 181 YEHTFFQAYYYCITLTITGFGDYVALQKDALQOTOPVYASFVYITLTLYTGAF 240  
 DB 181 CEEMSFHAYYYCITLTITGFGDYVALQKDALQKPLVYAFSMYITLVLTGYGAF 240  
 QY 241 LVVLRFTMNAEDKRDAAERHALLTRNGAQGGGGSAAHTPDASSPAAGGGCFRNV 300  
 DB 241 LVVLRFTMNAEDKRDAAERHALLTRNGAQGGGGSAAHTPDASSPAAGGGCFRNV 300  
 QY 301 -AEVLHFOQSMSCMLYKRSREKLOYSTIPMIPRDLSTDYCEGSHSPGGGRYSDTPSR 359  
 DB 301 -AEVLHFOQSMSCMLYKRSREKLOYSTIPMIPRDLSTDYCEGSHSPGGGRYSDTPSR 359  
 QY 359 KADVPDQSVSCSCYRSD--YGRSVAPQNSFSAKLAPHYRHSISYKIEISPSYTK 343  
 DB 344 NSLFP---SPISISPLHSTPHORLMKRKRSV 374  
 RESULT 10  
 ID AAEI3279 standard; Protein; 374 AA.  
 AC AAEI3279;  
 XX  
 DT 12-FEB-2002 (first entry)  
 XX  
 DE Human transporters and ion channels (TRICH)-6.  
 XX  
 KW Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;  
 KW diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;  
 KW cardiac disorder; angina; hypertension; myocarditis; hyperglycemia;  
 KW neurological disorder; Alzheimer's disease; cataract; infertility;  
 KW Wilson's disease; schizophrenia; Grave's disease; Addison's disease;  
 KW Huntington's disease; multiple sclerosis; meningitis; hypotensive;  
 KW cardiac; noctropic; neuroprotective; neuroleptic; ophthalmological;  
 KW antihypertoid; anticonvulsant; golitre; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /label- Signal\_peptide  
 FT Domain 26..374  
 FT /note- "Human mature TRICH6 protein"  
 FT 225..243  
 FT /label- Transmembrane\_domain  
 XX  
 PN W0200177174-A2.



PT activity -  
XX  
XX Claim 13; Fig 2; 123pp; English.

CC The present sequence is human TWIK-6 (G165) (Tandem of P domains in  
CC a Weak inward rectifying K<sup>+</sup> channel) protein. TWIK-6 DNA and  
CC protein are useful for treating potassium channel-associated disorders,  
CC central nervous system (CNS) disorders (Parkinson's disease, Alzheimer's  
CC disease, dementia, Huntington's disease, senile dementia, Gilles de la  
CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,  
CC progressive supranuclear palsy, epilepsy, Jakob-Creutzfeldt disease),  
CC autonomic function disorders (hypertension, sleep disorders, depression,  
CC neuropsychiatric disorders, schizophrenia, anxiety disorders,  
CC Korsakoff's psychosis, mania, phobic disorders), learning or memory  
CC disorders (amnesia, age-related memory loss, attention deficit disorder,  
CC dysrhythmic disorder, major depressive disorder, obsessive-compulsive  
CC disorder, psychoactive substance use disorders, anxiety, phobias, panic  
CC disorder), bipolar affective disorder (migraine, obesity), cardiovascular  
CC system disorders (arteriosclerosis, ischaemia, reperfusion injury,  
CC restenosis, arterial inflammation, vascular wall remodelling, ventricular  
CC remodelling, rapid ventricular packing, coronary microembolism,  
CC tachycardia, bradycardia, pressure overload, aortic bending, coronary  
CC artery ligation, vascular heart disease, atrial fibrillation, coronary  
CC syndrome, Lange-Nielsen syndrome, long-QT syndrome, congestive heart  
CC failure, sinus node dysfunction, angina, heart failure, hypertension,  
CC atrial fibrillation, atrial flutter, dilated cardiomyopathy, idiopathic  
CC cardiomyopathy, myocardial infarction, coronary artery disease and spasm,  
CC arrhythmias), musculoskeletal system disorders (paralysis, muscle weakness  
CC ataxia, myotonia and myokymia), cellular growth, differentiation or  
CC cell division disorders (cancer, carcinoma, sarcoma or leukaemia, tumour  
CC angiogenesis and metastasis, skeletal dysplasia, neuronal deficiencies  
CC resulting from impaired neural induction and patterning).  
CC neurodegenerative disorders, hepatic disorders, cardiovascular disorders  
CC and haematopoietic and/or myeloproliferative disorders. TWIK-6 DNA is  
CC useful in gene therapy.  
XX  
XX Sequence 400 AA:

Query Match 41.4%; Score 846; DB 22; Length 400;  
Best Local Similarity 64.7%; Pred. No. 2.8e-83;  
Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCFYLLVGAANFDALSEPELIERORLELROQELRARNYSOGYE 60  
DB 71 MRRPSVRAAGLVLTCLLYLGAANFDALSEBESGRRLVQKRGALRRKFGSAEDYR 130  
QY 61 ELERVVLRLLKPKHAGVQWRFAGSFYEALVTITIGYHAAPSTDGKVCMEFYALLGIPL 120  
DB 131 ELERLALQAEHPHRRAGRWKPFGSFEYFALTITIGYHAAPSTDGKVCMEFYALLGIPL 190  
QY 121 TLVWFOSLGERINTLVRLRLRAKKGICMRADYSMMAMVLIQFSCSTLCIGAAASH 180  
DB 191 TLVWFOSLGERLNNAVRLLLAAKCCGLRMTCVSTENLVVAGLACATATLGAVAASH 250  
QY 181 YEHYTFQAYYYCFITLTITIGFDVVALQKDAOTQPOYVAFSEVYLLTGLTVGALIN 240  
DB 251 FEGMWFYFAYYYCFITLTITIGFDVVALQKDAOTQPYVAFSEVYLLTGLTVGALIN 310  
QY 241 LVYLRFTMADEKRDRA 258  
DB 311 LVYLRFTVASADWPERAA 328

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AAB47334  
ID AAB47334 standard; Protein; 330 AA.  
XX  
XX AAB47334;  
AC  
XX  
XX 29-AUG-2001 (first entry)  
DT  
XX  
XX ECRR11.  
DE  
XX

KW FCTR1; energy metabolism; adipose storage; muscle mass;  
KW insulin secretion; glucose utilization; serum lipid level;  
KW triglyceride; cholesterol; human; diabetes; metabolic disturbance;  
KW obesity; metabolic syndrome X; anorexia; infectious disease;  
KW cancer-associated cachexia; cancer; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorder; dyslipidemia.

OS Homo sapiens.

FN Key Location/Qualifiers  
FN Peptide 1..23  
FN Protein /label= Signal peptide  
FN 24..330  
FN /label= Mature protein

MO200146231-A2.

28-JUN-2001.

21-DEC-2000; 2000MO-US34898.

21-DEC-1999; 99US-0171329.

20-DEC-2000; 2000DS-0171329.

(CURA-) CURAGEN CORP.

Burgess CE;

WPI; 2001-418026/44.

N-PSDB; AAC86163.

PT Novel FCTR1 polypeptides useful for treating, diagnosing and preventing  
PT diabetes, anorexia, obesity, cancer, neurodegenerative disorders,  
PT immune disorders and various lipidemias  
XX  
XX Claim 1; Page 31; 116pp; English.

CC This sequence shows a FCTR1 protein. The DNA sequence originates  
CC in chromosome 20. The FCTR1 protein is a novel K<sup>+</sup> channel-like  
CC protein and has a high probability of being sorted to the plasma  
CC membrane. The FCTR1 DNA was found to have 641 of 854 bases (75%),  
CC in a complete coding sequence of 2590 bases, identical to a human  
CC mRNA sequence encoding TWIK-related acid-sensitive K<sup>+</sup> channel (TASK).  
CC The FCTR1 protein has 168 of 258 residues (65%), identical to, and  
CC 200 of 258 residues (77%) positive with, mouse CTBAK having a total  
CC of 409 amino acids.

CC Note: This sequence is given as it is decoded from the corresponding  
CC DNA sequence. The specification includes additional amino acid  
CC sequences which are not encoded by the FCTR1 DNA.

CC FCTR1 polypeptides and associated nucleic acids are useful for  
CC treating or preventing a FCTR1-associated disorder related to  
CC energy metabolism in an organism that effects adipose stored, muscle  
CC mass, insulin secretion, glucose utilization and serum lipid levels  
CC including, triglycerides and cholesterol in human. These disorders  
CC include diabetes, metabolic disturbances associated with obesity,  
CC the metabolic syndrome X, anorexia, wasting disorders associated with  
CC chronic diseases, metabolic disorders, obesity, infectious disease,  
CC cancer-associated cachexia, cancer, neurodegenerative disorders,  
CC Alzheimer's disease, Parkinson's disorder, immune disorders,  
CC haematopoietic disorders, and various dyslipidemias.

XX Sequence 330 AA:

Query Match 41.0%; Score 838; DB 22; Length 330;  
Best Local Similarity 64.3%; Pred. No. 1.6e-82;  
Matches 166; Conservative 32; Mismatches 60; Indels 0; Gaps 0;

QY 1 MKRONVRLALIVCFYLLVGAANFDALSEPELIERORLELROQELRARNYSOGYE 60  
DB 1 MRRPSVRAAGLVLTCLLYLGAANFDALSEBESGRRLVQKRGALRRKFGSAEDYR 60  
QY 61 ELERVVLRLLKPKHAGVQWRFAGSFYEALVTITIGYHAAPSTDGKVCMEFYALLGIPL 120



Db 61 ELERLALQAPHRAGQMKPGSEFYAITVITTTIEGHAPGDSKVCFMFALLGIPL 120  
QY 121 TVMFGSLGRINTLVRYLLHRKKGIGMRADYSNANVLI GFSCISTLTGIAAFSH 180  
Db 121 TLVTFQSLGRNLNAVVRLLAAKCCIGRMTCVSTENLVAGLLCAATLALGAVAFSH 180  
QY 181 YEHMTFFQAYYYCFITLTITIGFDYVALQKDALQOPQVYAFSVYITLGLTVIGAFIN 240  
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QY 241 LVVLRFTMNADEKRD 258  
Db 241 LVVLRFLVASADMPERRA 258  
RESULT 13  
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ID AAE10678 standard; Protein; 400 AA.  
XX AAE10678;  
AC AAE10678;  
XX 18-DEC-2001 (first entry)  
XX Human TWIK-6 (E 165) protein.  
XX Human: Tandem of P domains in a Weak Inward rectifying K+ channel-6;  
KM TWIK-6: sensory nervous system disorder; cardiac; cellular proliferation;  
KM hemotopoietic; cytosolic; nocotropic; osteopathic; gene therapy; mania;  
KM vaccine; potassium channel-associated disorder; Parkinson's disease;  
KM Alzheimer's disease; dementia; Huntington's disease; multiple sclerosis;  
KM amyotrophic lateral sclerosis; hypertension; depression; inflammation;  
KM anxiety; amnesia; neuropsychiatric disorder; migraine; obesity; cancer;  
KM arteriosclerosis; ischaemia; cardiomyopathy; myocardial infarction;  
KM ataxia; arrhythmia; paralysis; muscle weakness; cellular growth; tumour;  
KM carcinoma; leukaemia; hepatic disorder; gene therapy.  
XX Homo sapiens.  
XX OS  
XX Key Location/Qualifiers  
FT Domain 75..144  
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FT /label= Transmembrane\_domain  
FT 78..96  
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FT 81..312  
FT /note= "Potassium channel protein domain"  
FT Domain 150..166  
FT /label= P-loop\_domain  
FT /note= "Pore-loop domain"  
FT 178..195  
FT /label= Transmembrane\_domain  
FT /label= Transmembrane\_domain  
FT 229..248  
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FT Domain 260..278  
FT /label= P-loop\_domain  
FT /note= "Pore-loop domain"  
FT 290..314  
FT /label= Transmembrane\_domain  
XX MO200166743-A2.  
XX 13-SEP-2001.  
XX 02-MAR-2001; 2001MO-US06933.  
XX PF  
XX 03-MAR-2000; 2000US-0518866.  
XX PR  
XX (MILL-) MILLENNIUM PHARM INC.  
XX PA  
XX Curtis RAJ, Glucksmann MA;  
XX PI  
XX WPI, 2001-596835/67.  
XX DR  
XX N-PSDB; AAD17525.  
XX

XX Novel TWIK-6 polypeptide of TWIK family of potassium channels for  
PT treating sensory nervous system disorders, cardiac-related disorders  
PT and cellular proliferation disorders comprises the modulation of its  
PT activity -  
PS Claim 13; Fig 1; 123pp; English.  
XX The present sequence is human TWIK-6 (E165) (Tandem of P domains  
CC in a Weak Inward rectifying K+ channel) protein. TWIK-6 DNA and  
CC protein are useful for treating potassium channel-associated disorders,  
CC central nervous system (CNS) disorders (Parkinson's disease, Alzheimer's  
CC disease, dementia, Huntington's disease, senile dementia, Gilles de la  
CC Tourette's syndrome, multiple sclerosis, amyotrophic lateral sclerosis,  
CC progressive supranuclear palsy, epilepsy, Jakob-Creutzfeldt disease),  
CC autonomic function disorders (hypertension, sleep disorders, depression,  
CC neuropsychiatric disorders, schizophrenia), learning or memory  
CC disorders (amnesia, age-related memory loss, attention deficit disorder,  
CC dysrhythmic disorder, major depressive disorder, obsessive-compulsive  
CC disorder, psychoactive substance use disorders, anxiety, phobias, panic  
CC disorder), bipolar affective disorder (mania, obesity), cardiovascular  
CC system disorders (arteriosclerosis, ischaemia, reperfusion injury,  
CC restenosis, arterial inflammation, vascular wall remodeling, ventricular  
CC remodeling, rapid ventricular packing, coronary microembolism,  
CC tachycardia, bradycardia, pressure overload, aortic bending, coronary  
CC artery ligation, vascular heart disease, atrial fibrillation, coronary  
CC syndrome, Lange-Nielsen syndrome, long-QT syndrome, congestive heart  
CC failure, sinus node dysfunction, angina, heart failure, hypertension,  
CC atrial fibrillation, atrial flutter, dilated cardiomyopathy, idiopathic  
CC cardiomyopathy, myocardial infarction, coronary artery disease and spasm,  
CC arrhythmia), musculoskeletal system disorders (paralysis, muscle weakness  
CC ataxia, myotonia and myokymia), cellular growth, differentiation or  
CC migration disorders (cancer, carcinoma, sarcoma or leukaemia, tumour  
CC angiogenesis and metastasis, skeletal dysplasia, neuronal deficiencies  
CC resulting from impaired neural induction and patterning),  
CC neurodegenerative disorders, hepatic disorders, cardiovascular disorders  
CC and haematopoietic and/or myeloproliferative disorders. TWIK-6 DNA is  
CC useful in gene therapy.  
XX  
SQ Sequence 400 AA:  
QY 1 MKRONRTLALVCTFTYLLVGAAYDALESEBELERORLELRARVNLGGYE 60  
Db 71 MRRPSVRAAGLVCTCYLLVGAAYDALESESESGRRLVQKRALRRKFGFSADYR 130  
QY 61 ELERVVLRKPKHAGVQMRFGAGSFYAITVITTTIEGHAPSDGKVCMEFALLGIPL 120  
Db 131 ELERLALQAPHRAGQMKPGSEFYAITVITTTIEGHAPGDSKVCMEYFALLGIPL 190  
QY 121 TVMFGSLGRINTLVRYLLHRKKGIGMRADYSNANVLI GFSCISTLTGIAAFSH 180  
Db 191 TLVTFQSLGRNLNAVVRLLAAKCCIGRMTCVSTENLVAGLLCAATLALGAVAFSH 250  
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Db 251 FEGMTFFHAYYCFITLTITIGFDYVALQSGEALQKRLPYVAFSFLYITLGLTVIGAFIN 310  
QY 241 LVVLRFTMNADEKRD 258  
Db 311 LVVLRFLVASADMPERRA 328  
RESULT 14  
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ID AAE13286 standard; Protein; 400 AA.  
XX AAE13286;  
AC AAE13286;  
XX







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:18:47 ; Search time 27 Seconds

(without alignments)  
429.357 Million cell updates/sec

Title:

US-09-939-484-4

Perfect score:

2042

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Total number of hits satisfying chosen parameters: 262574

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Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	2042	100.0	394	US-09-144-914-4	Sequence 4, Appl1
2	1819	89.1	405	US-09-144-914-5	Sequence 5, Appl1
3	370	18.1	370	US-09-144-914-8	Sequence 8, Appl1
4	369	18.1	411	US-09-236-080-6	Sequence 6, Appl1
5	363	17.8	411	US-09-236-080-2	Sequence 2, Appl1
6	363	17.8	411	US-09-336-643A-83	Sequence 83, Appl1
7	329.5	16.1	393	US-09-432-470-2	Sequence 2, Appl1
8	329.5	16.1	393	US-09-432-470-4	Sequence 4, Appl1
9	320.5	15.7	336	US-08-749-816-2	Sequence 2, Appl1
10	320.5	15.7	336	US-09-144-914-2	Sequence 2, Appl1
11	295.5	14.5	313	US-09-336-643A-81	Sequence 81, Appl1
12	253	12.4	336	US-08-332-312-4	Sequence 4, Appl1
13	231.5	11.3	618	US-08-332-312-2	Sequence 2, Appl1
14	190.5	9.3	383	US-08-749-816-4	Sequence 4, Appl1
15	190.5	9.3	383	US-09-144-914-7	Sequence 7, Appl1
16	176.5	8.6	107	US-09-236-080-4	Sequence 4, Appl1
17	156	7.6	347	US-08-749-816-3	Sequence 3, Appl1
18	156	7.6	347	US-09-144-914-6	Sequence 6, Appl1
19	131.5	6.4	646	US-09-336-643A-10	Sequence 10, Appl1
20	113	5.5	197	US-09-336-643A-16	Sequence 16, Appl1
21	112.5	5.5	1082	US-09-336-643A-20	Sequence 20, Appl1
22	112.5	5.5	1082	US-09-600-776-2	Sequence 2, Appl1
23	112.5	5.5	1083	US-09-143-494-1	Sequence 1, Appl1
24	111.5	5.5	636	US-09-142-791A-2	Sequence 2, Appl1
25	111.5	5.5	636	US-09-178-109-4	Sequence 4, Appl1
26	111.5	5.5	655	US-09-142-791A-4	Sequence 4, Appl1
27	111.5	5.5	655	US-09-178-109-2	Sequence 2, Appl1

28	105.5	5.2	636	4	US-09-142-791A-6	Sequence 6, Appl1
29	103	5.0	532	1	US-08-288-405A-10	Sequence 10, Appl1
30	102.5	5.0	626	2	US-08-956-242-2	Sequence 2, Appl1
31	102.5	5.0	626	3	US-09-351-215-2	Sequence 2, Appl1
32	99.5	4.9	494	1	US-08-464-340A-4	Sequence 4, Appl1
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34	99.5	4.9	888	2	US-08-956-242-4	Sequence 4, Appl1
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36	97.5	4.8	289	4	US-09-372-422A-14	Sequence 14, Appl1
37	97.5	4.8	1017	4	US-09-600-776-6	Sequence 6, Appl1
38	97	4.8	255	4	US-09-342-084-11	Sequence 11, Appl1
39	95.5	4.7	282	4	US-09-372-422A-8	Sequence 8, Appl1
40	95.5	4.7	288	4	US-09-372-422A-12	Sequence 12, Appl1
41	94	4.6	807	4	US-09-177-650-3	Sequence 3, Appl1
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44	94	4.6	1159	4	US-09-226-012-2	Sequence 2, Appl1
45	94	4.6	1159	4	US-09-226-012-4	Sequence 4, Appl1

#### ALIGNMENTS

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RESULT 1
US-09-144-914-4
; Sequence 4, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS. THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6/05CIP
; CURRENT APPLICATION NUMBER: US/09/144.914
; EARLIER FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749.816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095.234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 394
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: TASK
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Best Local Similarity 100.0%; Pred. No. 4.9e-218;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKRQNVRLALIVCTFYLLVGAAYFDALSEPELIERORLELROOELRARNLSOGGYE 60
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11 MKRQNVRLALIVCTFYLLVGAAYFDALSEPELIERORLELROOELRARNLSOGGYE 60
|||||
61 ELERVVLTKPKHKGAVQVRFGSFYEATVTITTYGHAAPSTDGKVFQCMFYALGLPL 120
|||||
61 ELERVVLTKPKHKGAVQVRFGSFYEATVTITTYGHAAPSTDGKVFQCMFYALGLPL 120
|||||
61 ELERVVLTKPKHKGAVQVRFGSFYEATVTITTYGHAAPSTDGKVFQCMFYALGLPL 120
|||||
121 TLVPOSIGERINTLVRLHRAKKGKLRADYSAMAMVLIQFSCISTLCIGAARSH 180
|||||
121 TLVPOSIGERINTLVRLHRAKKGKLRADYSAMAMVLIQFSCISTLCIGAARSH 180
|||||
181 YEHWFQAYYYCFTLTITIGFGDYVALQKDALOTOPQYVAFSFTVYLTGLTVIGAFLN 240
|||||
181 YEHWFQAYYYCFTLTITIGFGDYVALQKDALOTOPQYVAFSFTVYLTGLTVIGAFLN 240
|||||
Db 181 YEHWFQAYYYCFTLTITIGFGDYVALQKDALOTOPQYVAFSFTVYLTGLTVIGAFLN 240
|||||
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QY 241 LVVLRFTMNAEDEKRDABERALLTRNGAGGGGGGSAHTTDTASTAAAGGFFRNYY 300  
DB 241 LVVLRFTMNAEDEKRDABERALLTRNGAGGGGGGSAHTTDTASTAAAGGFFRNYY 300  
QY 301 AEVLHQSOMSCWYKREKLOYSIPMIIPROLDSTDCVEGSHSSGGGGRSDPSRR 360  
DB 301 AEVLHQSOMSCWYKREKLOYSIPMIIPROLDSTDCVEGSHSSGGGGRSDPSRR 360  
QY 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394  
DB 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394

## RESULT 2

US-09-144-914-5  
; Sequence 5, Application US/09144914  
; Patent No. 6309855  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lesage, Florian  
; APPLICANT: Fink, Michel  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
; FILE REFERENCE: 989, 6705CIP  
; CURRENT APPLICATION NUMBER: US/09/144, 914  
; EARLIER FILING DATE: 1998-09-01  
; EARLIER APPLICATION NUMBER: 08/749, 816  
; EARLIER FILING DATE: 1996-11-15  
; EARLIER APPLICATION NUMBER: 60/095, 234  
; EARLIER FILING DATE: 1998-08-04  
; EARLIER APPLICATION NUMBER: FR 96/01565  
; EARLIER FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 405  
; TYPE: PRF  
; ORGANISM: Murine  
; FEATURE:  
; OTHER INFORMATION: TASK  
US-09-144-914-5

Query Match 89.1%; Score 1819; DB 4; Length 405;  
Best Local Similarity 88.1%; Pred. No. 2, 8e-193;  
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

QY 4 QNRTALIVCTFTYLLVGAAYPDALSEPELIERQRLROQLRARNYLSGGYELE 63  
DB 1 ENRTALIVCTFTYLLVGAAYPDALSEPELIERQRLROQLRARNYLSGGYELE 60  
QY 64 RVLRLKPKHAGVQMFAGSFYFAITVITIGYHAPSTDGKVCMPFALLGIPITLV 123  
DB 61 RVLRLKPKHAGVQMFAGSFYFAITVITIGYHAPSTDGKVCMPFALLGIPITLV 120  
QY 124 MFQSLGERINTLVRYLLHRAKGLGMRADVSNANVLIQFSCISTLIGAAAFSHYER 183  
DB 121 MFQSLGERINTLVRYLLHRAKGLGMRADVSNANVLIQFSCISTLIGAAAFSHYER 180  
QY 184 WFEFOAYVVCFTLTITIGEDVVALOKDQALOTOPQVAFSFYITLGLVIGAFNLVY 243  
DB 181 WFEFOAYVVCFTLTITIGEDVVALOKDQALOTOPQVAFSFYITLGLVIGAFNLVY 240  
QY 244 LRFMTNAEDEKRDABERALLTRNGAGGGG-----GSAHTTDTASTAA----- 291  
DB 241 LRFMTNAEDEKRDABERALLTRNGAGGGG-----GSAHTTDTASTAA----- 291  
QY 292 --GGGGRFNVYAEVLHQSOMSCWYKREKLOYSIPMIIPROLDSTDCVEGSHSSPGG 349  
DB 301 GVGSGFRNVYAEVLHQSOMSCWYKREKLOYSIPMIIPROLDSTDCVEGSHSSPGG 360  
QY 350 GGVSTPFRRCCLSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394  
DB 350 GGVSTPFRRCCLSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394

DB 361 GGVSTPFRRCCLSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 405

## RESULT 3

US-09-144-914-8  
; Sequence 8, Application US/09144914  
; Patent No. 6309855  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lesage, Florian  
; APPLICANT: Fink, Michel  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
; FILE REFERENCE: 989, 6705CIP  
; CURRENT APPLICATION NUMBER: US/09/144, 914  
; EARLIER FILING DATE: 1998-09-01  
; EARLIER APPLICATION NUMBER: 08/749, 816  
; EARLIER FILING DATE: 1996-11-15  
; EARLIER APPLICATION NUMBER: 60/095, 234  
; EARLIER FILING DATE: 1998-08-04  
; EARLIER APPLICATION NUMBER: FR 96/01565  
; EARLIER FILING DATE: 1996-02-08  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 370  
; TYPE: PRF  
; ORGANISM: Murine  
; FEATURE:  
; OTHER INFORMATION: TREK-1  
US-09-144-914-8

Query Match 18.1%; Score 370; DB 4; Length 370;  
Best Local Similarity 31.6%; Pred. No. 1, 6e-32;  
Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRONVTLALIVCTFTYLLVGAAYPDALSEPELIERQRLROQLRARNYLSGGYELE 60  
DB 42 MKKRVSTIPLVY--VLVLIIGAAYFKALEPQPEISQRTIVIQKQFTIAHQCVNS--T 97  
QY 61 ELERVVRL-KPKHAGV-----QMRFGSYFAITVITIGYHAPSTDGKVCY 108  
DB 98 ELDELQOIVAAINAGIIPLGNSNOVSHDLSSEFFAGTITVITIGFNGISPRTEGKI 157  
QY 109 FCFEVALIGIPLVLFQSLGERINTLVRYLLHRAKGLGMRAD-----VSM 156  
DB 158 FCIITVALLGIPLEGFLAGVGDQGITF-----GKIAYEDTFTKMYNSQTKIRI 208  
QY 157 ANNVLIGFSCISTLIGAAAFSHYERWTFEFOAYVVCFTLTITIGEDVVALOKDQALOT 216  
DB 209 ISTIIFILGCVLFVALPAVIFKHIGWSALDAIYFVITLITIGEDVYAGSD--IEV 266  
QY 217 QPOYVAFSFYITLGLVIGAFNLVY--VLRFMTNAEDEKRD-ABERALLTRN 267  
DB 267 LDEYKPVVFWMLVGLAYFAVLSMIGDWLRVTSKTKKEVGEFRAHAAEWMTAN 320

## RESULT 4

US-09-236-080-6  
; Sequence 6, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: NO. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236, 080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 411

TYPE: PRT  
ORGANISM: Mus musculus  
US-09-236-080-6

Query Match 18.1%; Score 369; DB 4; Length 411;  
Best Local Similarity 31.0%; Pred. No. 2.4e-32;  
Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

OY 1 MKRONVRLALIVCTFTYLLVGAADFALSEPELIERORLELROOELRARNLSOGGYE 60  
DB 42 MKMKTSTIFLVV-VLTLIGATVFKALDEPHEISQRTTIVIOKOTFISQHCYNS--T 97  
OY 61 ELERVVLR-KPHKGV-----QWRPAGSFYATVITTTIGYGHAPSNDGKV 108  
DB 98 ELDELIOQIVAINAGIIPLGNTSSNOVSHMDGSSFFRAGTVITTTIGGNISPRTEGGKI 157  
OY 109 FCMFYALLGIPPLTFMPOSIGERINTLVRYLLHRAKKGIGMRAD-----VSM 156  
DB 158 FCIYVALLGIPPLFGFLAGVGDQGTIF-----GKGIKAVEDFTIKMNVSOIKIRI 208  
OY 157 ANMVLIGFSCISTICIGAAAFSHYEHMTFFOAYVYCTTTTTFGSDYVALOKDOALOT 216  
DB 209 ISTIIFILFGCVLFALPAVIFKHEGMSALDAIFVYITTTTIGFGDYVAGGSD--IEY 266  
OY 217 OPOYVAFSVYILTGLTVIGAFNLV--VLRFMTNABDEKRD-AEHRALLTRN 267  
DB 267 LDFYKPVVFWILVGLAFVAFVLSMIGDMLRVISKKEEVEGEFRHAHAEMWTAN 320

RESULT 5  
US-09-236-080-2  
Sequence 2, Application US/09236080

GENERAL INFORMATION:  
APPLICANT: Helen Meadows  
TITLE OF INVENTION: No. 642217e1 Compounds  
FILE REFERENCE: GP30031  
CURRENT APPLICATION NUMBER: US/09/236,080  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-236-080-2

Query Match 17.8%; Score 363; DB 4; Length 411;  
Best Local Similarity 31.0%; Pred. No. 1.1e-31;  
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

OY 1 MKRONVRLALIVCTFTYLLVGAADFALSEPELIERORLELROOELRARNLSOGGYE 60  
DB 42 MKMKTSTIFLVV-VLTLIGATVFKALDEPHEISQRTTIVIOKOTFISQHCYNS--T 97  
OY 61 ELERVVLR-KPHKGV-----QWRPAGSFYATVITTTIGYGHAPSNDGKV 108  
DB 98 ELDELIOQIVAINAGIIPLGNTSSNOVSHMDGSSFFRAGTVITTTIGGNISPRTEGGKI 157  
OY 109 FCMFYALLGIPPLTFMPOSIGERINTLVRYLLHRAKKGIGMRAD-----VSM 156  
DB 158 FCIYVALLGIPPLFGFLAGVGDQGTIF-----GKGIKAVEDFTIKMNVSOIKIRI 208  
OY 157 ANMVLIGFSCISTICIGAAAFSHYEHMTFFOAYVYCTTTTTFGSDYVALOKDOALOT 216  
DB 209 ISTIIFILFGCVLFALPAVIFKHEGMSALDAIFVYITTTTIGFGDYVAGGSD--IEY 266  
OY 217 OPOYVAFSVYILTGLTVIGAFNLV--VLRFMTNABDEKRD-AEHRALLTRN 267  
DB 267 LDFYKPVVFWILVGLAFVAFVLSMIGDMLRVISKKEEVEGEFRHAHAEMWTAN 320

RESULT 6  
US-09-336-643A-83  
Sequence 83, Application US/09336643A

GENERAL INFORMATION:  
APPLICANT: Miller, Andrew P.  
APPLICANT: Curran, Mark Edward  
APPLICANT: Hu, Ping  
APPLICANT: Ruter, Marc  
APPLICANT: Wang, Jian-Wang  
TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels  
FILE REFERENCE: SEQ-15P  
CURRENT APPLICATION NUMBER: US/09/336,643A  
PRIOR FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: 60/076,687  
PRIOR FILING DATE: 1998-08-07  
PRIOR APPLICATION NUMBER: 60/116,448  
PRIOR FILING DATE: 1999-01-19  
PRIOR APPLICATION NUMBER: PCT/US99/03826  
PRIOR FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 83  
LENGTH: 411  
TYPE: PRT  
ORGANISM: H. sapiens  
US-09-336-643A-83

Query Match 17.8%; Score 363; DB 4; Length 411;  
Best Local Similarity 31.0%; Pred. No. 1.1e-31;  
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

OY 1 MKRONVRLALIVCTFTYLLVGAADFALSEPELIERORLELROOELRARNLSOGGYE 60  
DB 42 MKMKTSTIFLVV-VLTLIGATVFKALDEPHEISQRTTIVIOKOTFISQHCYNS--T 97  
OY 61 ELERVVLR-KPHKGV-----QWRPAGSFYATVITTTIGYGHAPSNDGKV 108  
DB 98 ELDELIOQIVAINAGIIPLGNTSSNOVSHMDGSSFFRAGTVITTTIGGNISPRTEGGKI 157  
OY 109 FCMFYALLGIPPLTFMPOSIGERINTLVRYLLHRAKKGIGMRAD-----VSM 156  
DB 158 FCIYVALLGIPPLFGFLAGVGDQGTIF-----GKGIKAVEDFTIKMNVSOIKIRI 208  
OY 157 ANMVLIGFSCISTICIGAAAFSHYEHMTFFOAYVYCTTTTTFGSDYVALOKDOALOT 216  
DB 209 ISTIIFILFGCVLFALPAVIFKHEGMSALDAIFVYITTTTIGFGDYVAGGSD--IEY 266  
OY 217 OPOYVAFSVYILTGLTVIGAFNLV--VLRFMTNABDEKRD-AEHRALLTRN 267  
DB 267 LDFYKPVVFWILVGLAFVAFVLSMIGDMLRVISKKEEVEGEFRHAHAEMWTAN 320

RESULT 7  
US-09-432-470-2  
Sequence 2, Application US/09432470

GENERAL INFORMATION:  
APPLICANT: David Malcolm Duckworth  
APPLICANT: Conrad Gerald Chapman  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP-30190  
CURRENT APPLICATION NUMBER: US/09/432,470  
PRIOR FILING DATE: 1999-11-03  
EARLIER APPLICATION NUMBER: UK 9923668.9  
PRIOR FILING DATE: 1999-10-07  
EARLIER APPLICATION NUMBER: UK 9824048.4  
PRIOR FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 393  
TYPE: PRT





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? REGISTRATION NUMBER: P-38,711
? REFERENCE/DOCKET NUMBER: 32,422
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-831-3246
? TELEFAX: 201-831-3305
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS
? LENGTH: 336 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-332-312-4

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Query Match	12.4%	Score 253;	DB 1;	Length 336;
Best Local Similarity	30.3%	Pred. No. 1.3e-19;		
Matches 61;	Conservative 39;	Mismatches 51;	Indels 50;	Gaps 8

```

QY      69  LKHHKAGVOMRFSGSYEFALITVITIGGHAAPSDGKVCMTVALGIPLLVPMOSL 128
Db      19  VKNAATETMTWTFSSSIEFAVTVVLTIGVGNPVPVTNIGRMICLFESLLGIPLLVTADL 78
QY      129  GERI-----NTL-VRYLL--HRAKK-----GLG-----MRADYSMA 157
Db      79  AGKFLSEHLVWLYGNLTKLKYLLLSRHRKEREHREHCEHSHGMDHNIIEKRIPAFV 138
QY      158  NMVLIGFSCISITLCIGAAPSFHYEHMTFFQAYYICFTTLTGTGGVVALOKKOALQTO 217
Db      139  LALLIAY-----TAGGVLMKRLKLPSPFSFYSFVSMFTMTVVGQDLMF-RRP----- 185
QY      218  PQRVAFSEFVILNGLVIGAF 238
Db      186  -----GYMIIILVLTILGKF 200

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RESULT 13

US-08-332-312-2

; Sequence 2, Application US/08332312  
; Patent NO. 5559026

GENERAL INFORMATION:  
APPLICANT: Price, Laura A.  
APPLICANT: Pausch, Mark H.  
TITLE OF INVENTION: Functional Expression of a Drosophila  
TITLE OF INVENTION: Melanogaster Putative Potassium Channel in Yeast  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/332,312  
FILING DATE:

US-08-332-312-2

Query Match	11.3%	Score 231.5	DB 1	Length 618
Best Local Similarity	23.1%	Pred No. 8.1e-17		
Matches 94	Conservative 76	Mismatches 150	Indels 87	Gaps 16

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QY      RTALILVCFETYLALGAAAFDALIESEPELIEHQRLLELQDLRLARYNLSSGGVEEL-----62
Db      5 RWILLILFIYSILMFCAALYHIEHGEKIS-----RAEGRKQAIAMINELYLEELGDN 58

QY      63 -----ERVNLR-----KP-----HKAGVQMRFGSYFAIYITTIIGHAAPSIDCG 106
Db      59 TTQDEILQRIISYCDKPVTLPTDYDDTPYTWTFFAHAFVAFVCSYVGCGNISPTTFAG 118

QY      107 KVCMEFYALIGIPILVLMVQSLGEBINILNRLRLHRAK-----GIGMRADY 154
Db      119 RMLMIVSYAIGIPVNCILFAGLGEFFGRTFEATYRKYKMYKMSDHYVPPQGL---1 174

QY      155 SMANWVLIFFQSCISPL-CIGAAAFSHEHMTFFQAVYCCFCTITLTIGFGDY-ALOKQD 212
Db      175 TTYVAILINGIALFLVLPVCYVHLNR--ELGISLSILYISVYTTTITIGFGDYVTFBQD 232

QY      213 ALQTOPQYVAFSFVYILTLGVLIGAFMLVYLRFETNAAEDEKRDAAERALLFRNGQAGG 272
Db      233 PKFEGGMFVYQIVFVIMFIFSLGL--VMIMTFITRLQSKILAYLEQD-----281

QY      273 GGGGSAHHTDITASSTAALAAAGGGGFERNYAENVLHDSQMSCILMYISREKLQYS---IPMI 329
Db      282 -----SSNIAKATQNRIMSGVPMEDVGYLRRLMNEL-YILTKVPYTVTDVIAYTL 328

QY      330 PRDLSTSDPCVDEGSHSPGGGGRYDTPSR---CLCS---GARSA 370
Db      329 PRNSQSPDLSTMYRVEPAP-----ISPRKAESVCDNMGAAQREA 367

```

## RESULT 14

US-08-749-816-4

; Sequence 4, Application US/08749816  
: Patent No. 6013470

GENERAL INFORMATION:  
APPLICANT: Lesage, Florian  
APPLICANT: Guillemaire, Eric  
APPLICANT: Fink, Michel  
APPLICANT: Duprat, Fadrice  
APPLICANT: Lazdunki, Michel  
APPLICANT: Romey, Georges  
APPLICANT: Barhault, Jacques  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,  
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING  
TITLE OF INVENTION: OF DRUGS  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WEISER & ASSOCIATES  
STREET: 230 South Fifteenth Street, Suite 500  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102  
COMPUTER READABLE FORM:



TELEFAX: 215-875-8394  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 383 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-749-816-4

Query Match 9.3%; Score 190.5; DB 3; Length 383;  
Best Local Similarity 24.0%; Pred. No. 1.4e-12;  
Matches 62; Conservative 48; Mismatches 95; Indels 53; Gaps 9;

QY 11 LIVCTFTYLLVGAVFDALESEPELIERORLELROQLRANV--NLSSG---GYELE-- 63  
DB 44 LVLSCTVYALGGAVLFSLIEHPLEKREKAIREFODLKQOFMGNITSGIENSQSIET 103  
QY 64 --RVLRRLK-PHKAGV-----QWRFAGSFYFAITVTITIGYHAAPSTDGK 107  
DB 104 TKRLILMLDANHNHAFEFYFLNHEIPKDMTFSSALVFTTIVIPGYGIFFVSAYGR 163  
QY 108 VFCEFYALLGIPLTLVNFOSIGERINFLVRYLLHRAKKGLGMRADVSMANV----- 160  
DB 164 MCLIAVYALLGIPLTLVNMADTGKFAQLV-----TRMFGDNMNAIPALFYCLLPAYP 216  
QY 161 -LIGFSCISITLCIGAAAFSHYEHMTFEOAYVYCFITLTITGFGDYVALQKDALQTOPO 219  
DB 217 LVVGFILCSITS-----NITYLDSYFSLSTISITIGFGD---LTPDMNVIHMYL 261  
QY 220 YVAFSPYIILGLTVIGA 237  
DB 262 FLAVGVILVTTLDIVAA 279

## RESULT 15

US-09-144-914-7  
Sequence 7, Application US/09144914  
Patent No. 6309855  
GENERAL INFORMATION:  
APPLICANT: Duprat, Fabrice  
APPLICANT: Lesage, Florian  
APPLICANT: Lazdunski, Michel  
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
FILE REFERENCE: 989.6705CIP  
CURRENT APPLICATION NUMBER: US/09/144,914  
EARLIER FILING DATE: 1998-09-01  
EARLIER APPLICATION NUMBER: 08/749,816  
EARLIER FILING DATE: 1996-11-15  
EARLIER APPLICATION NUMBER: 60/095,234  
EARLIER FILING DATE: 1996-08-04  
EARLIER APPLICATION NUMBER: FR 96/01565  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 383  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog  
US-09-144-914-7

Query Match 9.3%; Score 190.5; DB 4; Length 383;  
Best Local Similarity 24.0%; Pred. No. 1.4e-12;  
Matches 62; Conservative 48; Mismatches 95; Indels 53; Gaps 9;

QY 11 LIVCTFTYLLVGAVFDALESEPELIERORLELROQLRANV--NLSSG---GYELE-- 63  
DB 44 LVLSCTVYALGGAVLFSLIEHPLEKREKAIREFODLKQOFMGNITSGIENSQSIET 103

QY 64 --RVLRRLK-PHKAGV-----QWRFAGSFYFAITVTITIGYHAAPSTDGK 107  
DB 104 TKRLILMLDANHNHAFEFYFLNHEIPKDMTFSSALVFTTIVIPGYGIFFVSAYGR 163  
QY 108 VFCEFYALLGIPLTLVNFOSIGERINFLVRYLLHRAKKGLGMRADVSMANV----- 160  
DB 164 MCLIAVYALLGIPLTLVNMADTGKFAQLV-----TRMFGDNMNAIPALFYCLLPAYP 216  
QY 161 -LIGFSCISITLCIGAAAFSHYEHMTFEOAYVYCFITLTITGFGDYVALQKDALQTOPO 219  
DB 217 LVVGFILCSITS-----NITYLDSYFSLSTISITIGFGD---LTPDMNVIHMYL 261  
QY 220 YVAFSPYIILGLTVIGA 237  
DB 262 FLAVGVILVTTLDIVAA 279

Search completed: July 1, 2003, 15:22:53  
Job time : 29 secs

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